STRUCTURE OF EVERNINOMICIN (ZIRACIN)

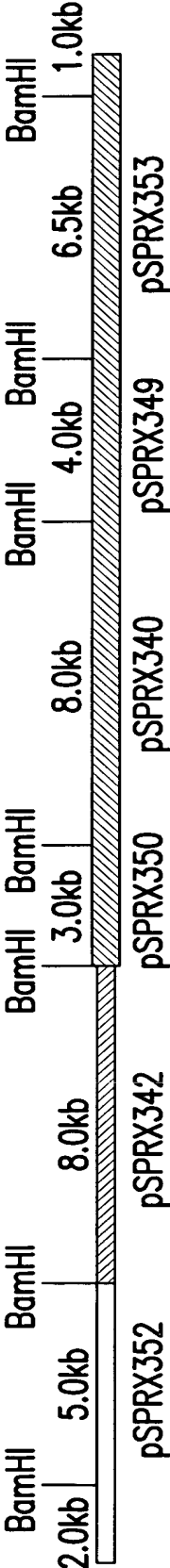ORSELLINIC ACID

GLYCOSYL GROUPS

ORSELLINIC ACID

FIG. 1

pSPRX272
37.5kb

COSMID pSPRX272

REGIONS SEQUENCED INDICATED
BY CROSSHATCHES.

FRAGMENTS CLONED INDICTED
BY CLONE DESIGNATION BENIGTH
FRAGMENT.

pSPRX272
(37500 bp)

FIG.2B

COSMID pSPRX256

REGIONS SEQUENCED INDICATED
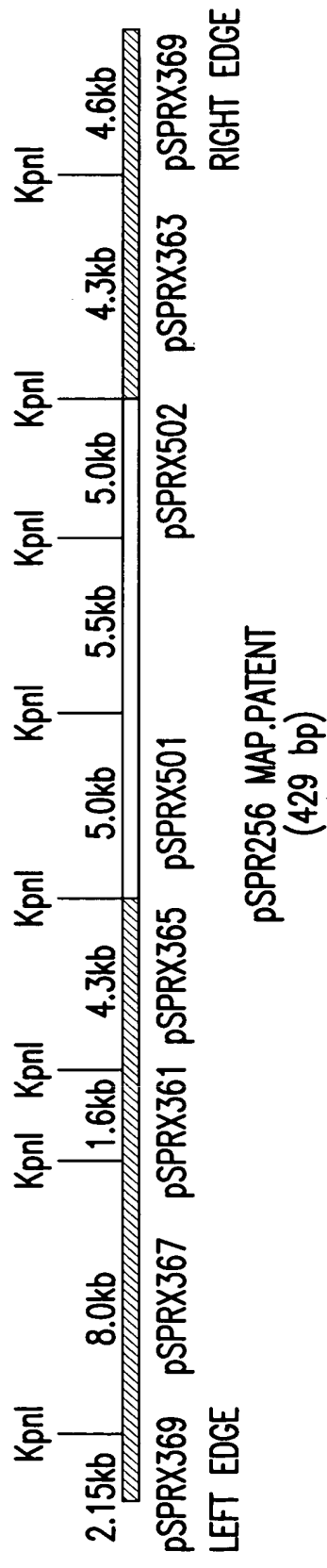BY CROSSHATCHES.

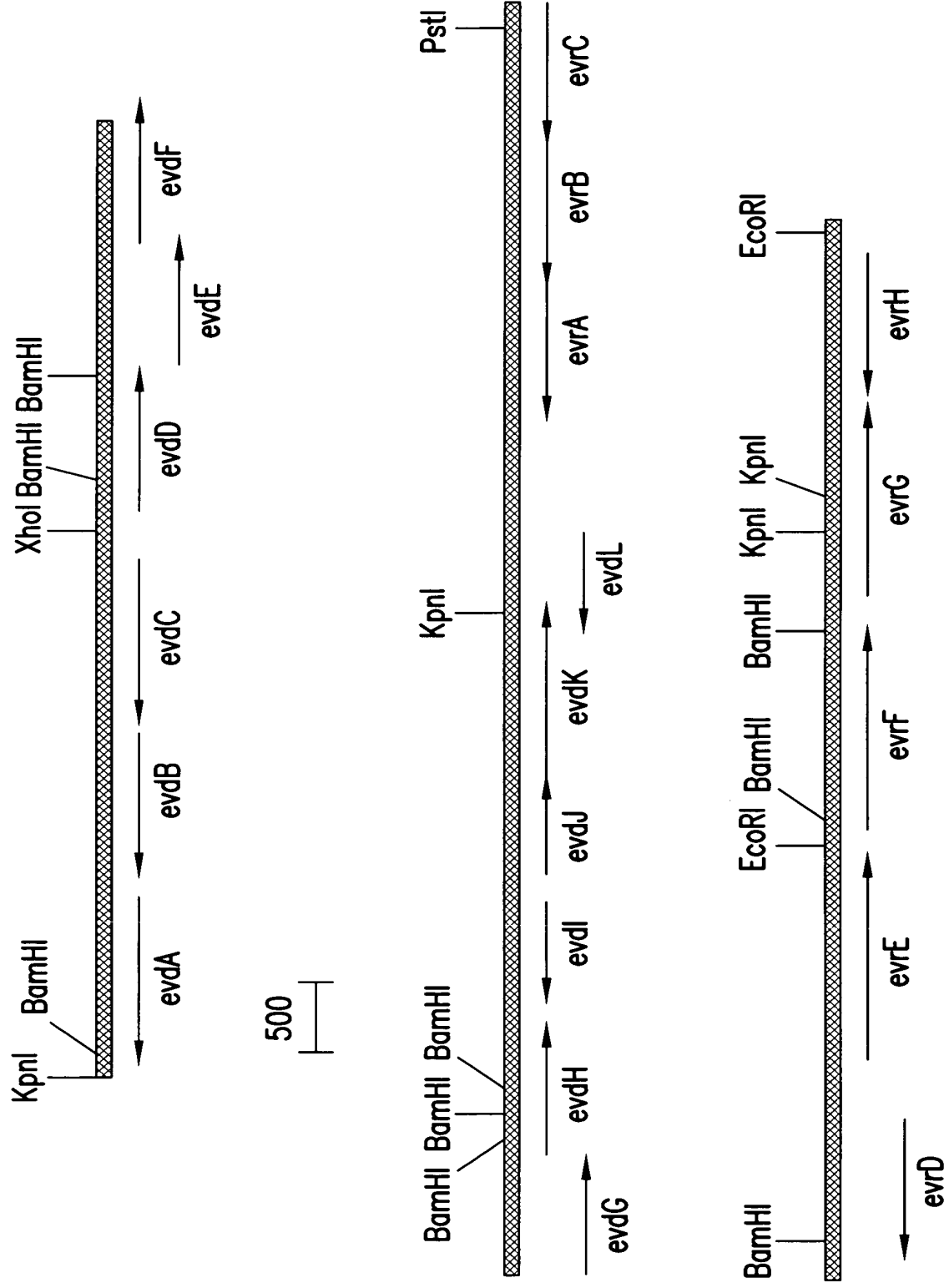FRAGMENTS CLONED INDICATED
BY CLONE DESIGNATION BENIGTH
FRAGMENT.

COSMID
pSPRX256

FIG.2C

FIG.3A

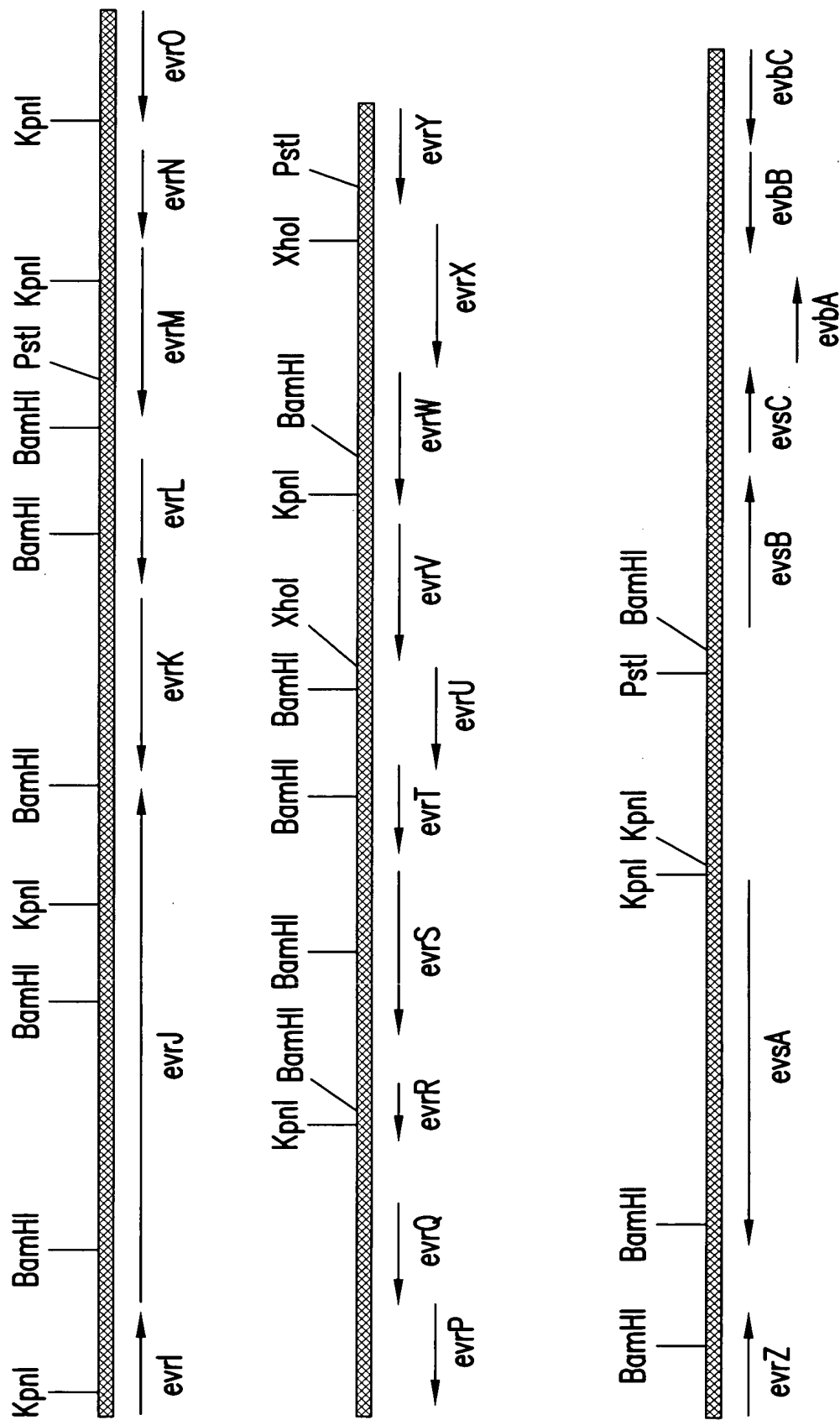FIG.3B
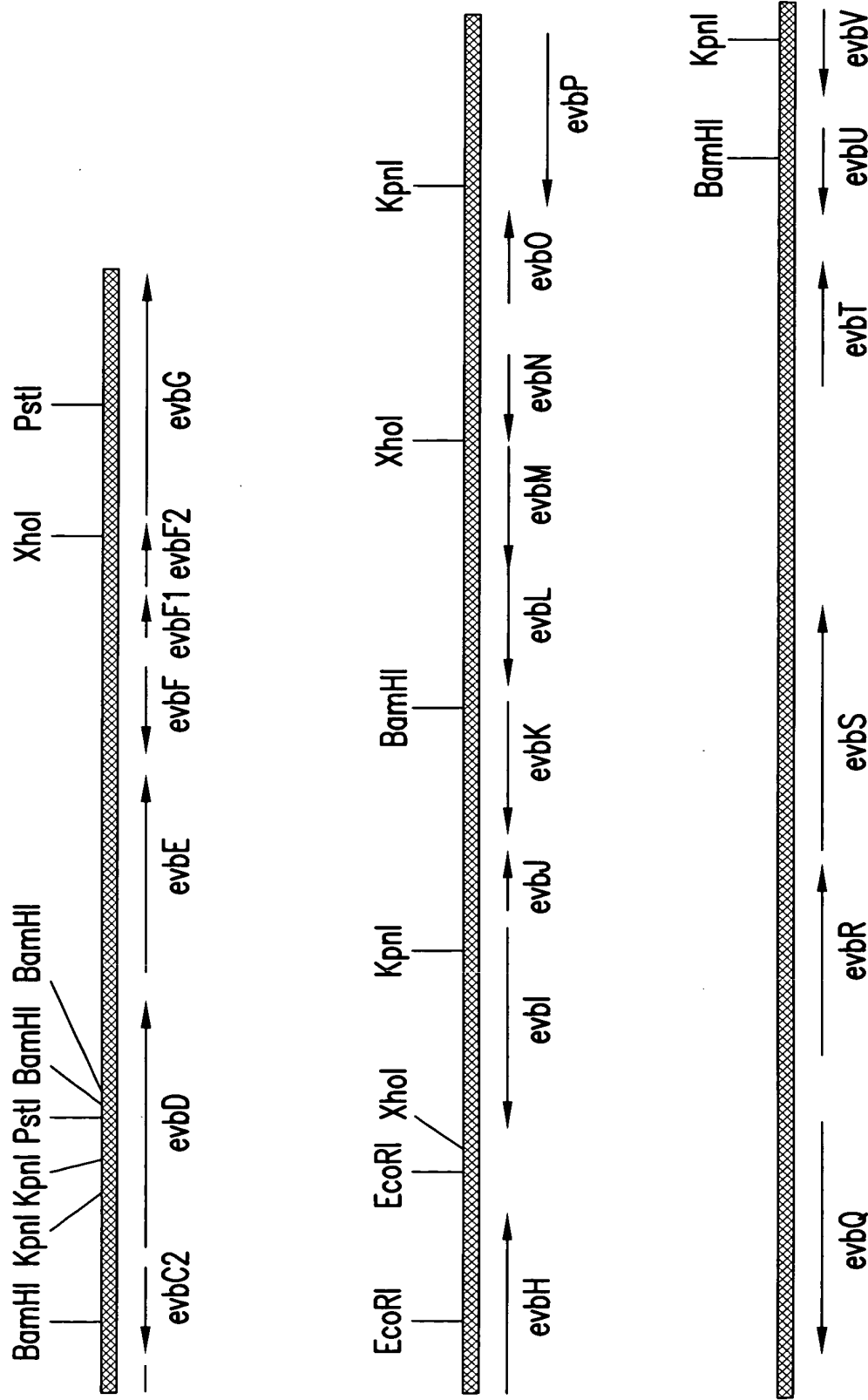
FIG.3C
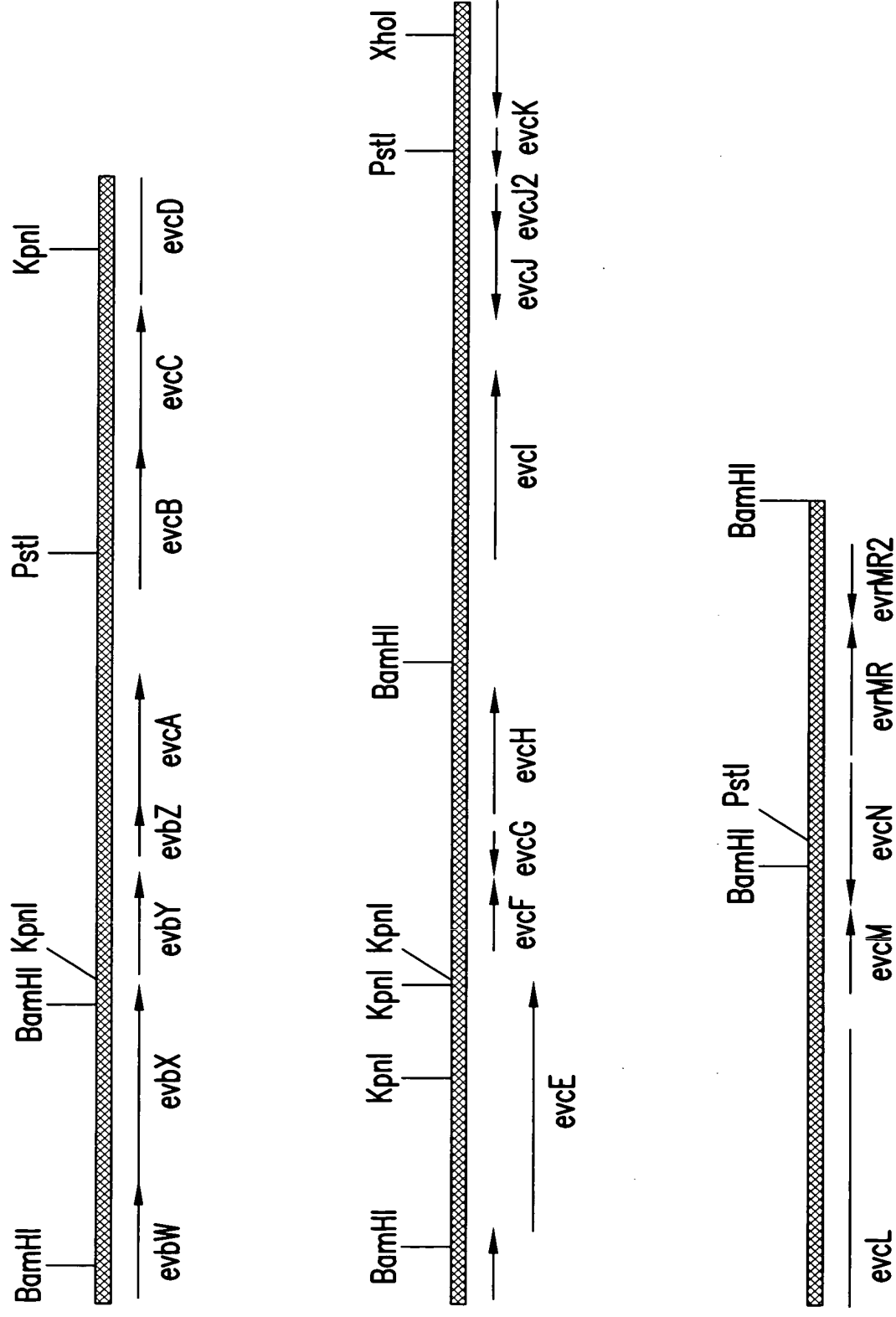
FIG.3D
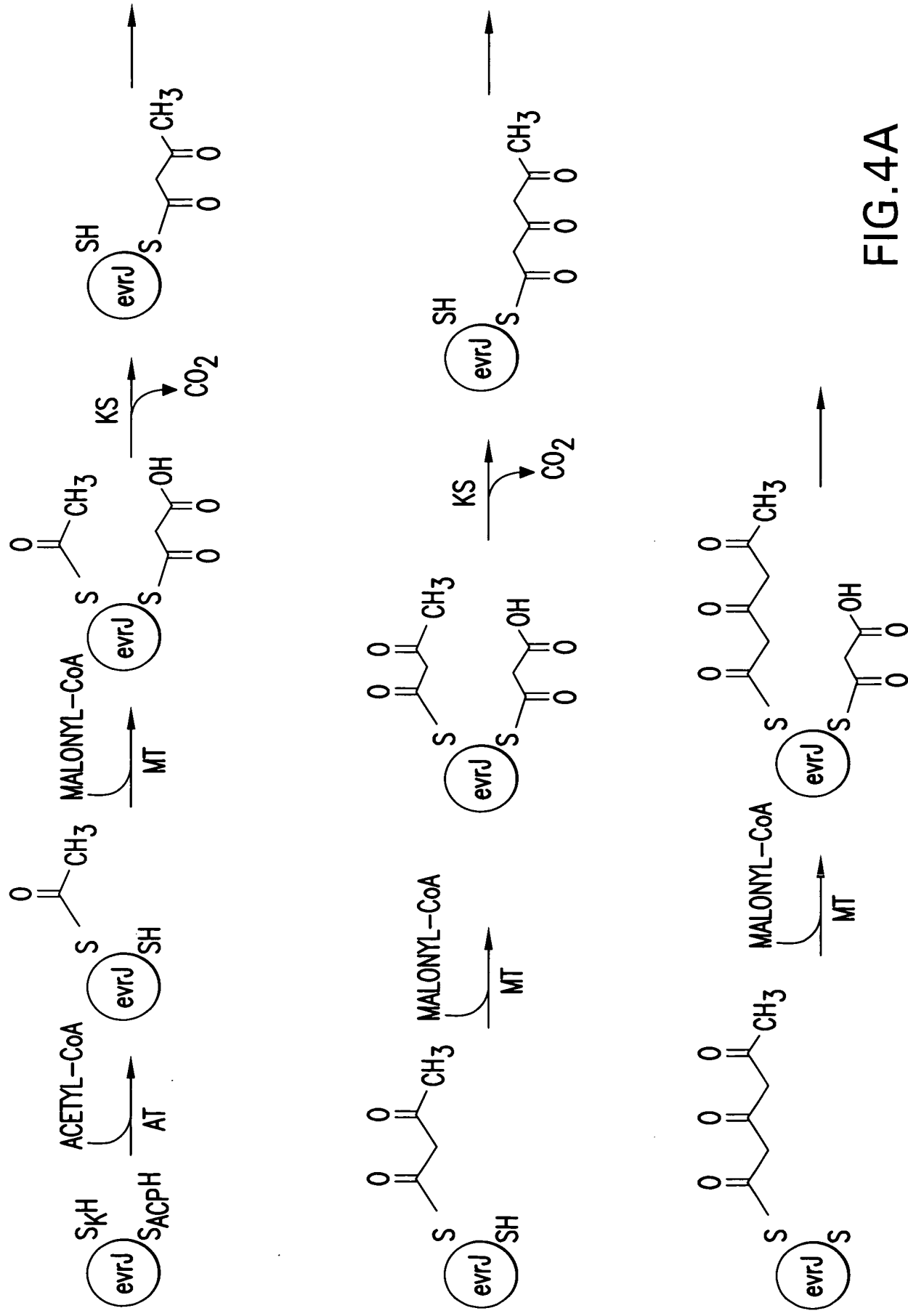
FIG.4A
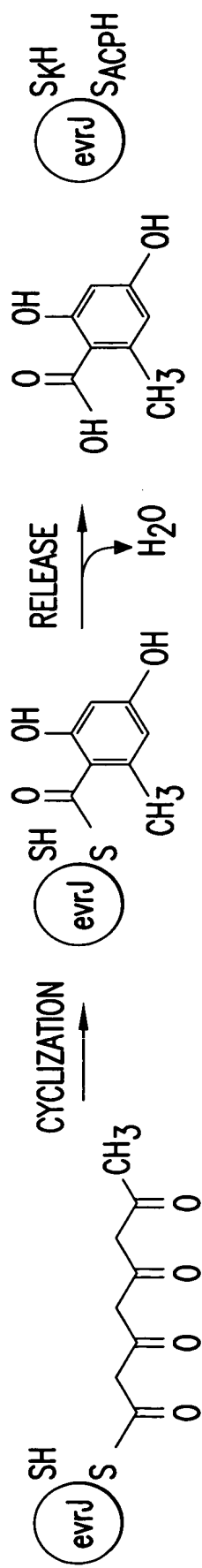
FIG.4B

pSPRH830b *E.coli*-MICROMONOSPORA SHUTTLE VECTOR
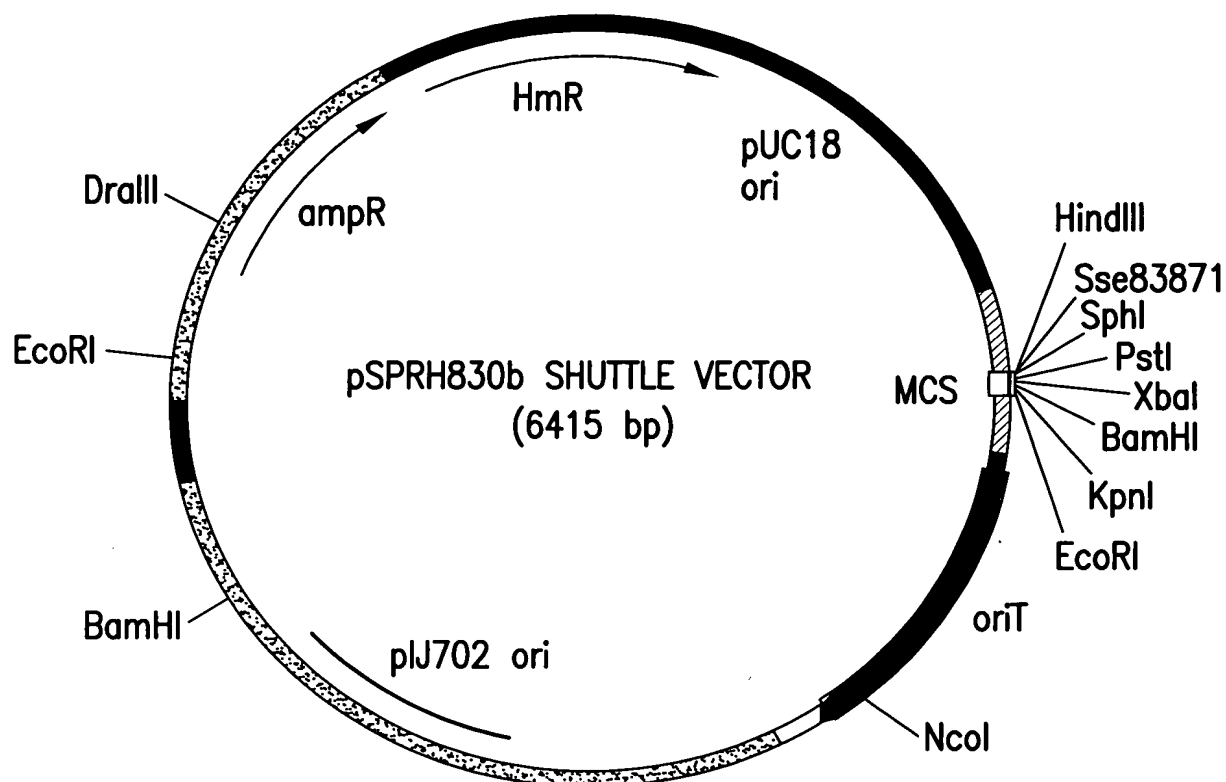
pSPRH830b − pSPRH826b BACKBONE

FUNCTION	SOURCE
− AMPICILLIN RESISTANCE	(pUC18)
− MULTIPLE CLONING SITE	(pUC18)
− pUC18 ORIGIN	(pUC18)
− HYGROMYCIN RESISTANCE	(p16R1)
oriT (ORIGIN OF TRANSFER)	(pRL1058)
pIJ702 ORIGIN OF REPLICATION	(pIJ702)

FIG.6

pSPRH840 INTEGRATING VECTOR

pSPRH840
(7098 bp)

HYGROMYCIN
RESISTANCE

XLS

INTEGRASE

oriT   INVERTED
REPEAT
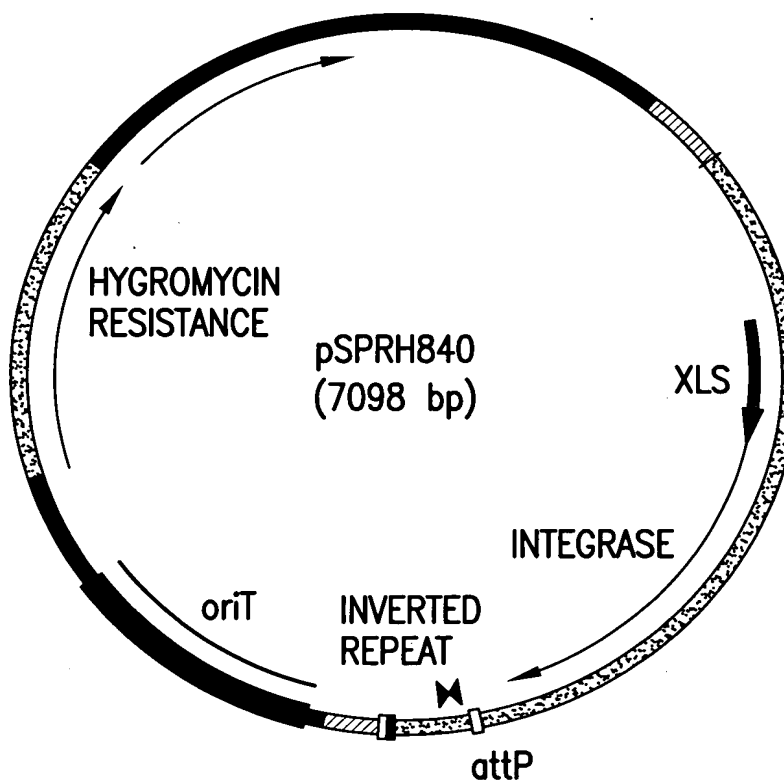
attP

pSPRH840 − pSPRH826b BACKBONE, pMLP1 *xis*, *int* attP INSERT

pSPRH840 CONJUGATED
FROM *E.coli* INTO   HmR TRANSFORMANTS OBTAINED

M.CARBONACEA   +

M.ROSARIA   −

M.HALOPHITICA   +

FIG.7A

1   GTACCTCGCCCTTGATCGTGCGGGTGGCCGGCTCGGCCGGCT?????TCGTGTGCGGGTAGGGTCTCGGGACATCTGGACTCCTTGCTTGCGGTAGGC?????CGGGTGGGAGCCTC

117 GGCCGGTGGTGCGGTGGGGGCTCGTCTGGCGTCTGCGTCAGGCCGCAGCCAGCCCGGCGGGGTGGTCCCGCGCGGGGGCTTGGCGCTTGATCGGTCCGGCGCCCTCGGCGGGTTG

233 GTGGGGGCGCGGGAGGGGGGAGAGCTCGGCTTTTTCGGGCACGTGATCGGCACGGGTCCGGGCGGGTCGGGAAGATGCCCGGCAGGGGTCGCGTCGCTCCTTCTTTGCTCTCAAGCCACGCAGGGGAT GTGTCGCTCTGTCGGAA

349 GCGGGGCGTGCCGGCCGAGACCCAGGTGATCGGCACGGGTCCGGGCGGTGATGGCGTGGCAGGGTCCGCGCCACGGCATGTGCAGGGCGGCGGCGGAGCTGCTCCTTGTTCATCAGCGGGCT

465 TCATGCGGCGGCCTCGAACAGGTCCTCGACCTTGGTGCCGAGCCGAGCAGTCGGGCCCATGTGCAGGGCCCCGAGGGGGCTCGGGGTCTGCCCCTTGCGGGATGCGGCAGCAGAGTTGACCCGAT

581 CCATGCCCGCACAGTCGCGGCCCCGAGGGGGCGGTTGGTGTCGAGGCCCAGGTTCGGGGCGGTCGAAGACGTCAGTGGCGTAGGCCGAATCGGCAGTGCGACGCACGTATGCGGCGATTG

697 ATCTCCGGGAGGTGCTGCACTCATGTCGCAAGCCTAGGGTGCTGCACTCGTGTCGCACCCTCGTACTTTCGGCCGATTCTGACCCGGCCCTCCAGGACCCTACTGTTGCATCAGTGCA

813 ACACCTATGAAGGAAGCAAGATGCCCGGCACGAGAGAGGAGATGGCGGTAGGCAAGCGACGATCAAGATGTGGAGCGCAGTGGTGTTGCGCAAAGGCAACGCGACAGGTCCGCAACC

929 GGTCCGACCTGCGCGGTTACGACCTACGGTGTGCACA**ATG**GGCAACACACCCGGGGCTGGGGCGGGCACATGGCCGCATACGTCCTCACCGCGCGGGAGCGCGGCACTGACCAAG
1►   M R N T P G L G R G T W A A Y V L T A R E R A G L T K

1044 AGCGAGTTGGCCAGGCGCATCCAGAAGGACCGCGCCACCGTCGGCCGGTGGGAGGACGGCAAGAACCGGCCCGACGAGGGGAAGCTCGTTGCCCGGGTCGCCCAGGTGCTCGGCCT
28► S E L A R R I Q K D R A T V G R W E D G K N R P D D A D L V A R V A Q V L G L

1160 CGACCTCGACGAAGCCCTCGCCGCGCCGGCGTCTGCGCCCCGGCGTCACCCCGCGACCCCAACCATGAGCCCAGCCCAACCCAGCTGG
66► D L D E A L A A A G L R P G V T P P A T P T M D L D E E I E L V R T D P K L

1276 ACGAGGAGACATGAAGCGGCGCATCATCGCCCTAATCCTGAGCGCGGGACAAGCGGCGGCGATCGAGGAGAAACCAAGCGGCTCATCGACCTGTTCCGCCGGAGC**TGA**CA
105► D E D M K R R I I A L I L E R R E R D K A A I E E T K R L I D L F R R S ◦

FIG.7B(1)

1391 ACGGTGTGGATCGAGAAGAACGGGCCGGTCTACCGCATTCGGGACCTCGTTCGAGAGACCGGTTATCCGAGGAGAGACCAGGGCGCCAAGAATGCGATGG
1▸ V W I E K N G P V Y R I R D L V R G K K V T I Q T G Y P T K T S A K N A M

1506 TGCAGTTCCGTGCGGAGCAGTTGCAGGGCAACGCGCTCATGCCGCGCGGCGGTCAGATTACCCTCGCCGATTTCGTGGGGGAGTGGTGGCCTAGAAAGACGCTGAAACCG
38▸V Q F R A E Q L Q G N A L M P R G G Q I T L A D F V G E W W P S Y E K T L K P

1622 ACGGCGGTGAACTCGGAGGGCAACGGCAACCGGATCGCGAACCACCTCCTGCCCATACTCGGCCATCTCACCCTTGACGAGCTGGACGGGCAGGTCACCCAGCAGTGGGTCAAGGACCTGGA
77▸ T A V N S E G N R I R N H L L P I L G H L T L D E L D G Q V T Q Q W V N D L E

1738 GGGCCGGGGTCGGCCCGTGGCCCGGAGTCCAGCGGGGTCGGGAAGCCGCTGGCCAGGAGAGGATCAGCAACTGCCACGGCCTGCTGCACGATCTGCGGGGGGATCGGCG
115▸ A G V G P W P E S T R G R R K P L A A K T I S N C H G L L H T I C G A A I A

1854 CGAAAACGGATCAGGCTCAACCCGTGCTCTTCGACGATGCTGGCCCCCCGGGCGGCCGACCCGGAGATCGAAGTTCCTGAGCGCCGAAAGAGATGAAGTTCCTGAGCCGCTTCGGCG
154▸A K R I R L N P C S S T M L P R R E P K E M K F L S D P E I G R L I T A L P P

1970 CACTGGCCGACCCGCCTGGTCATGCTGCTGGTGGCGACGGGTCTGAGGTGGGGTGAGGCGATCGGCCTGCGCGCGGGTCGGGCGCCGGTGACGGTCGT
193▸ H W R P L V M L L V A T G L R W G E A I G L R A G R V D L L A A R P R L T V V

2086 CGAGCAGCTCCAGGAGCTGGCCCAGAGACCGGAGAGCTCGTCTTCCAGTCGCCGAAGACGCCGGAAGGGCCGGGCCACGGTCAGTTTCACCACGAAAGTCGCTCTACTGCTTACGCCAC
231▸ E Q L Q E L A S T G E L V F Q S P K T A K G R R T V S F T T K V A L L L T P

2202 TCATCGCCGGAAAGAAGAAAGTGACGAGTCGTGTTCACCGGGCGGCGAAAGGCGGACATGGTAAGGACGCGGCAATTTCCGGCGGGATCTGGGTCAAGGCGTGCGAGGAAGCCGGCTTCCG
270▸L I A G K K S D E V V F T A P K G G M V R T N F R R I W V K A C E E A G L P

2318 GGCTTACGCGCATTCACGATCTGCGGCACACTCAGCGGGCGGCGATCCTGAATTTCTGCCGGCGGCTGCGTCGGCGGATCCCCGCGCGCTCGGTCGTGTCGGTCACGGATCT
309▸ G L R I H D L R H T H A A I L I S A G R P L S A I S R R L G H S S I A V T D L

FIG. 7B(2)

2434 GCTGTACGGGCACCTGGCTGGTGAGGAGGTCGACGAGGGGATCCTCGCGGCGATCGAGGAGGCGATGGCCGGCGGCGTCCGGGCTGAGGAGCTGGAGGCGGAACTCGACGAGGAGCTGACGG
347► L Y G H L R E E V D E G I L A A I E E A M A G V R A E D L E A E L D E E L T

2550 ACGTTGGTTGGCCGACGCAGCAGCATGATCAACTCTAGGGGAGAGGGGTAGGGGAATCCACTCCGGAGAGACGCCCGGAGCAACCAGCAGGTCAGGTGGCCTGT
386►D V L A D A A A •

2665 TGACCCCCTGACCAGGCGCCCCGGTACGGGGTTCAATTCCCATCAGTCACCCGGCAAGTGGATCTACTCCACAGCAGATCAGGCCCCTCCGAAGAGGGGCCTG

2768 ATGGGGTCATAGGGGGACAGGTAGGGGGAACTCAACCCCGGCTCCTTGCTCGGGTGCGGGTCATGCCGTCCGGTACCCCTCCGGTTCCTCGATCTCGGCG

2884 GCGAGCTGATCGGCGCAGAGGTGCGGCCTCCATCGCGTTCGGCCGTCTCGCCGGCGTTCGGAGGCCAGGACCCCGGCGCACTCGGCGGGCATGGCGGATCCGGCG

3000 CCAGGCGGGCGAACGGCCTCCGTCACGGCGCTCCAGCCGGCCTCCAGCCGCTCGTCGCGCTCGATGTGCGGCGGCCATCGGACTCGATGAGCGTCCTGGTAGT

3116 GCTCCCGCTCGTCGTCGCCACTGTCGCGGCGTCGGCGGGCGCGGCGCTGGCCAGCGGCTGCCAAGCGGCGGAGGGTGCAAGGATCATCGTGCTCATC

3232 ATGGGTCCGGTCTCCGATCAGGCGACCCCGGCGGGCGGGGCGGTGCGAGCGGCGGAGGGCGTGATCGTTTCGAGGATGGATGTACACCGGGTACTCCTCCAGGTTGGAGACTCGCCCTGCGATCAGAGACA

3348 CCCGTTCGACTGGTGACCGGAAAGCCTGCTCGCGGGAGGCCTGCTCGGGGAGGACTCCACCGGAGGACTTCCACGTGGTAAGGGTTACTCAGAGTGATGTTTCATAGGG

3464 TGGGGGCCGGTCGACAATGACGTAGAGTGGCCTTACCATGCACTTCCGTCGGTGGTAACCTGGACGTGTGCGTTACCGGTGCGGTAAGGCTGTGCGGAACAGGCG

3580 AACCCGGATCAGGCGGCGGAATGCGGCAGGCCTACCTCTCATCCGGCGGATATACATCCATCAGCCGTCCGGGACACCCTCGGGGATGTTCATCTC

3696 CGCTCGGCTCCTCCGGGCGTGGGCGCATCCGGGCCATGACGAACTGGTCCGGGCTCCGGTCGGAGTTCGACCGGCCCCAGCCTGGTGCCTCGCCCGGATGTGTTCATCGA

FIG.7B(3)

3812 CGAGTCCCTCAGGCGGCGCAGCTCGGCGACCGCCGTCGGCACGGTGCCCCTGCCCACCCGTACTCCTGGCTCAGCCGAGTCTCGCTGGGCAGCAGCCCGCCCAGCGTACGTGCCG

3928 TCCTGGATGCGGGGCGCGCAGCAGCGCGGCCAGCTGGAGGGGCGGCGGCCAGCTGGATCACACGGCCGGAGTGCGGGGCGGACGTTCGCCCGCGGCGCAA

4044 CGTTCGAACGTTCGGTGCGCTCTATGCCTCGGCCACAGTATACCCCTGCTCCGGCGGCGGCCCAGGGTAAGCCCGCGGGTCCCGGTGAGCTCCAGGGGCGGCGGCTGGATGGTCGACACGC

4160 TGACCGGAGTACAGATCGGCCAGCTCTCGCAGCGACGGGGAGCTTCGACCCGGCGGCGGGTACTCGCTGCTGCTGGGGATGCGGCGGCGGTCAGGTCGTCGGGCGGCGGATCTCGCCGCGGAGCGACGACATGGGG

4276 ATGGGCATGGCGCGGATCTCCCCTGGTTGGGCCCGCGGATGACATCACGGCCCGCCAGCGTGATTGACCAGTAGTCACACAGTGACCTAGGTTGGCCGGATGGGTAC

FIG.7B(4)

pSPRH826b INSERTION PLASMID
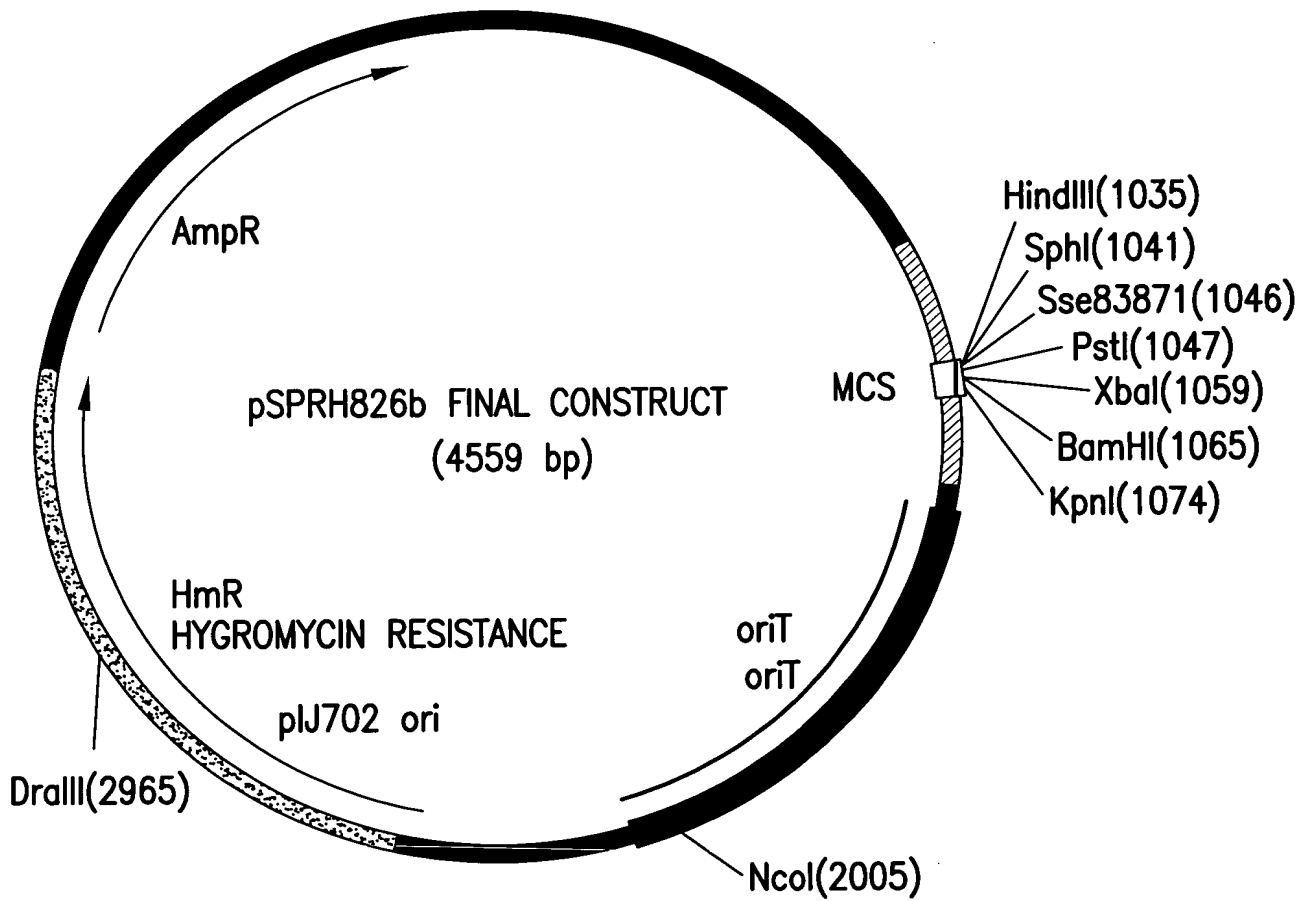
FIG.8

Analysis of *M. Carbonacea* and *M. Halophytica* pSPRH840 insertion site AttB/AttP region

Alignment of pMLP1 attP region with religation clone edge sequence

```
M. Halophytica PstI relig-9    TGATCAACTCTAGGGGAGGGGTAGGGGAATCCACTCCGGAGACGCCCGAGCAATCCGGA   60
M. Carb PstI relig-1           TGATCAACTCTAGGGGAGGGGTAGGGGAAT-CNCTCCGGAGACGCCCGAGCAATCCGGA   59
M. carb PstI relig-4           TGATCAACTCTAGGGGAGGGGTAGGGGAATCCACTCCGGAGACGCCCGAGCAATCCGGA   60
pMLP1.intTGA.att region        TGATCAACTCTAGGGGAGGGGTAGGGGAATCCACTCCGGAGACGCCCGAGCAATCCGGA   60

Consensus                      TGATCAACTCTAGGGGAGGGGTAGGGGAATCCNCTCCGGAGACGCCCGAGCAATCCGGA   60


M. Halophytica PstI relig-9    GCATGACGGAGCAACCAGCAGGTCAGGTGGCCTGTTGACCCCCTGACCCCGGTA   120
M. Carb PstI relig-1           GCATGACGGAGCAACCAGCAGGTCAGGTGGCCTGTTGACCCCCTGACCCCGGTA   119
M. carb PstI relig-4           GCATGACGGAGCAACCAGCAGGTCAGGTGGCCTGTTGACCCCCTGACCCCGGTA   120
pMLP1.intTGA.att region        GCATGACGGAGCAACCAGCAGGTCAGGTGGCCTGTTGACCCCCTGACCCCGGTA   120

Consensus                      GCATGACGGAGCAACCAGCAGGTCAGGTGGCCTGTTGACCCCCTGACCCCGGTA   120
```

FIG.9A(1)

M. Halophytica PstI relig-9   CGGGTTCAATTCCCATCAGTCACCCCAGGTAAGACCCAGGTCAGGGCCGGTTCTCACC-G 179
M. Carb PstI relig-1   CGGGTTCAATTCCCATCAGTCACCC---GT-ACACGAAGGCCCCCTCCAC-TCGGAGGGG 174
M. carb PstI relig-4   CGGGTTCAATTCCCATCAGTCACCC---GT-ACACGAAGGCCCCCTCCAC-TCGGAGGGG 175
pMLP1.intTGA.att region   CGGGTTCAATTCCCATCAGTCACCC---G--GCAAGTGGATCTACTCCACAGCAGATCAG 175

Consensus   CGGGTTCAATTCCCATCAGTCACCCCAGGTARSAMSHRGRYCHVSKCCRSWKCDSABSRG 180

M. Halophytica PstI relig-9   GCCCT-GACGGCATTTTCAGGGG------- 200
M. Carb PstI relig-1   GCCTTCGGCGGT-TCCTGAGGGTTCGCG-- 200
M. carb PstI relig-4   GCCTTCGGCGGT-TCCTGAGGGTTCGC--- 200
pMLP1.intTGA.att region   GCCCCCTCCG---AAGAGGGGGCCTGAT   200

Consensus   GCCYCKVCGYATYHWSAGGGKKCSYGAT   209

Insertion juncture

FIG.9A(2)

pMLP1 attP region

1 TGATCAACTCTAGGGGGAGGGGTAGGGGAATCCACTCCGGGAGACGCCCGGAGCAATCCGGAGCATGACGGAGCAACCAGCAGGTCAGGTGGCCT

94 GTTGACCCCCTGACCAGGGCCCCGGTACGGGGTTCAATTCCCATCAGTCACCCCGGCAAGTGGATCTACTCCACAGCAGATC

174 AGGCCCCCTCCGAAGAGGGGGCCTGATGCGTCATAGGGGACAGGTAGGGGAACTCAA

FIG.9B

CLONING SCHEME TO TEST POTENTIAL RESISTANCE GENES
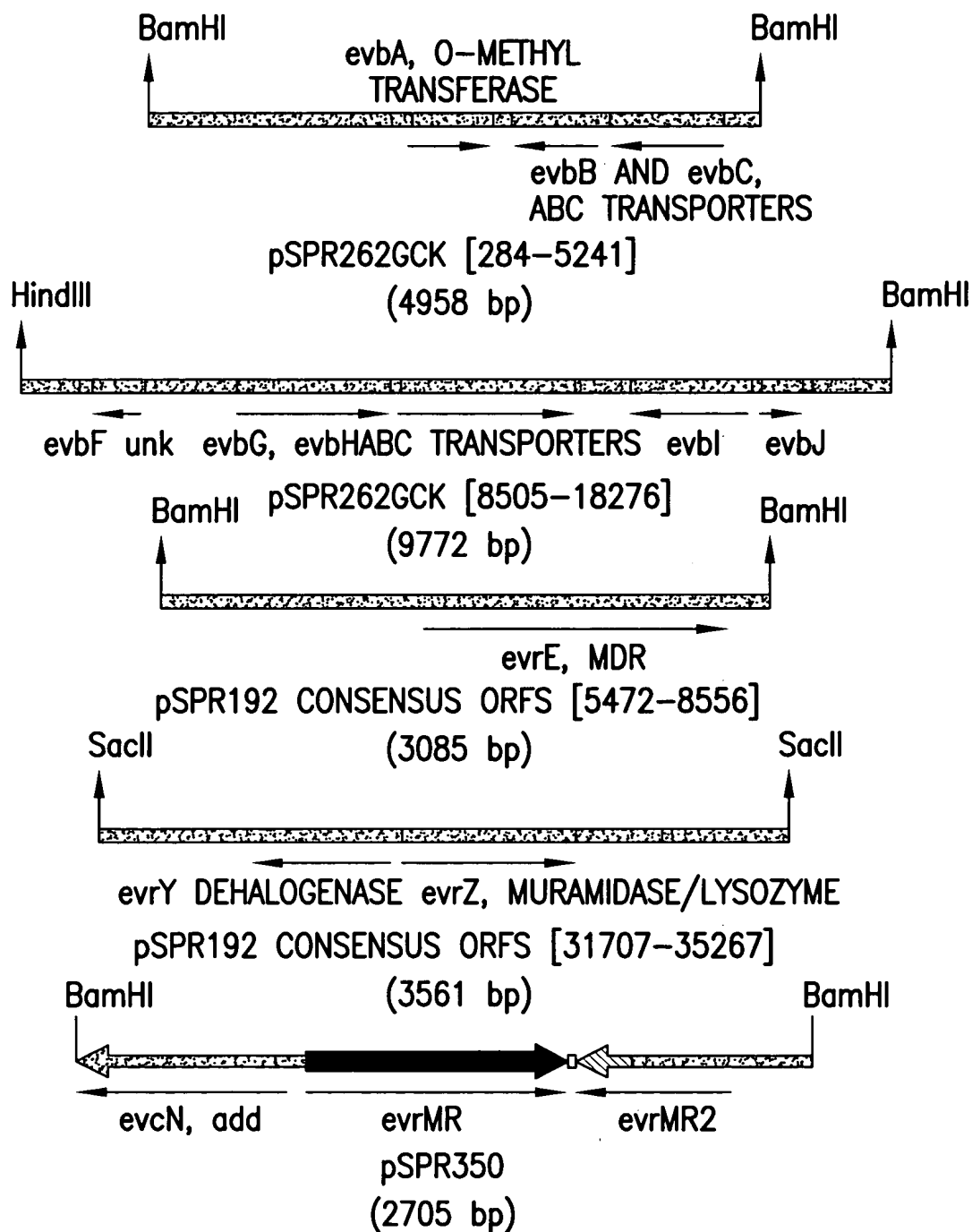
FIG.10

```
   1 GGTACCCGACCGTGTCCCGGAACAACGAGTCGAGATACGGCGGAGAGGAACACCCCCGGTAGTCCGGGTAGACGGTGGGCGCGAAGGCGTAC

  93 GCGCCTTCGACGGTCAGCGGGGCGGACACCGGCGGGGTCAGTCGTCACGTGTACGGGGGACGTACAGGATCCACTGTCCGCCAGCC
     < .   S  T  V  H  V  R  P  V  Y  L   I  W  Q  G  G  A

 184 CGGCGGAACTCCTGCTCCTTCGCCATGATCTCGTCGGCGTGGTTCCAGGGCGAAGAGCAGCGCGTAGTCCACCGGCGTCGGGCGTCGAACGCGTC
     <R  F  E  Q  E  K  A  M  I  E  D  A  H  N  W  A  F  L  L  A  Y  D  V  A  D  P  T  F  A  D

 276 CGGGGTGCGCACCGGGATGTGCTGCGGGGGTGAGCCCTGCTTGGCCGGCCTGTCTTGGCCGTAGTCCACCGGCGTCGGGCGTGAACGCGGACCGA
     <P  T  R  V  P  I  H  T  G  P  T  L  R  G  Q  K  A  P  T  T  D  C  V  W  S  V  L  D  P  G  I

 368 TGCCGCAGAAGTTCGTCACGGTGGCGCTCTTCGCCGTGCCACCACCCGCTTGCCCTCGGCCTTGAGCGAGTTCAGCAGGGCG
     <   G  C  F  N  T  V  T  A  S  K  A  T  A  G  Y  A  V  V  R  K  G  E  A  K  L  S  N  L  L  A

 460 AGCAGGTCGGTGCGGATGCCCTCGAGCGTCGGGGGCGGCGAACCTGTCGAGCCGGTCGGCGACCCTCGGGGGTCCTCGCGATCAG
     <L  L  D  T  R  I  G  E  V  D  A  A  F  R  D  L  R  S  R  D  A  V  G  R  A  D  E  E  G  I  L

 552 CGCGGGCCACCCGCTCGGCGCTCGCGCCGCCGCGATGGTGTAGCCGGCCGATGTGTAGGGCCGAGAAGGCGTTCCACGTCGA
     <A  A  V  R  E  A  P  Q  R  A  G  A  R  A  I  T  Y  R  V  E  G  G  H  V  P  L  R  E  V  D  V

 664 CGAGCGCGGAAGCCGAAGCGGGCCCAGCGCGTCGCCACGCGCCGCGAGAAGAAGAAATGCTCGTGTAGATCTGGTCGAAGGACGTC
     <   L  A  F  G  F  R  A  A  L  A  Q  V  S  R  A  S  F  F  F  H  E  D  Y  I  Q  D  F  S  T

 736 TTGTCCAGGATGTCCCGAGGTACGGGGTCCTCGAAGACGAAGACCCGTCAAGCCCCGGAGGATGGAGTGGAG
     <K  D  L  I  D  G  L  Y  P  D  E  F  V  F  V  G  D  P  A  L  L  A  D  V  G  R  L  I  S  D  L

 828 GTAGGGGATGTGGCAGATGGTGTTGGCCGCGAAGATCACATCGGCCAAGGGCCGTCTCCCTGACCCGGGGGGGTGGACTCCTCGAAGA
     <Y  P  I  H  C  I  T  N  A  A  F  I  V  D  A  P  G  D  T  E  R  V  R  R  A  T  S  E  E  F  F

 920 ACTCGGTGACCACCCGCACCCGTGCCCACGCGCCACCCGACGGCTCGAAGCCCAGGTGCGCCACTCCCGCCTCGTGG
     <   E  T  V  V  R  V  G  H  G  R  A  V  D  A  V  G  G  S  P  E  F  G  L  H  R  V  G  A  E  H

1012 ACGGTACGCAGCAGCATCACCCCGTCGTTGCAGCCGATCTCCACCACGAACAGGGTCCGGCGGCCGGTGCCGCGCGGT
     <V  T  R  L  M  V  G  D  N  C  G  I  E  V  V  F  P  D  P  G  T  A  E  H  E  L  L  H  R  A  T
```

FIG.11A(1)

```
1104 GTCGGGGAAGTGCTTCTGCATCACGGAGGAGCCCGACGAGTGGTACGGGGTAGTCCTGGTGGAACATCTCCTCCCGGGGCACCTCCTCCATGA
     <D  A  F  H  K  Q  M  V  S  S  G  S  S  H  Y  P  Y  D  Q  H  F  M  E  E  R  P  V  E  E  M  L

1196 GCTGCACCATGCTGCAGCCCGCGCAGCCCCACCGCCCAGGTGGAAGAAGAACTCGTCGGGAGCTGGTGCTCGGTGAGGAACCGGTGTCGGAG
     <Q  V  M  T  C  G  A  C  V  G  V  A  L  H  F  F  E  D  A  L  Q  D  E  T  L  F  R  D  S

1288 AGCGGGCTGCCGACCAGGTCGGGCGGTGGTCGCCGCCACACGCCCGGCCAGGTGCCGGGCGGTGCCGTCGGCTGAATCGGT
     <L  P  Q  R  G  L  D  L  F  Q  A  T  T  G  G  C  A  R  C  T  G  R  R  P  T  G  D  A  S  D  T

1380 CATCGGCATTCCTTCCATGGATACCCCTGCCTCAGGCAGGCGGATGTCAACGACGTCTCCTTGTCGGGATGGGTCGTCCAGCTCTCGGC
     <M

1469 TGCGGGCGTGCCGGCCGGCGACTCAGAGGCGCCGGAGCACGTCGGCGAGCGTCCTGCGTCTCCGGCGGCCAGCGAGGGA
     <·  L  A  A  L  V  D  R  L  A  D  I  V  R  D  Q  T  E  P  P  L  S  P

1560 TACATGGGGAGGGAGAAGATCTCGCCGCCAACCGTTCCGTGGTGGGGAGGGAGCCGGTCTGGTAGCCGGTCATGGT
     <Y  M  P  L  S  F  I  E  G  A  L  R  E  T  T  P  L  S  G  T  Q  Y  G  L  K  A  F  G  T  M  T

1652 GTGCACCGGCCAGGGGTAGCTGATGTTGAGCGCGTAGTCGGTGGGGTGGCGGGACCACGT
     <H  V  P  W  P  Y  S  I  N  L  A  I  D  R  A  A  L  Q  E  L  I  R  D  R  A  P  H  R  V  V  Y

1744 AGACGTACCAGACGTGTTGTCGGTGTTCGGCGCCGGTCACCGGGTCAGGCGGATGTCGGCCAGCCCTCTCGTAGCGC
     <V  Y  W  H  E  N  D  T  A  T  V  P  L  T  L  G  V  Q  D  A  I  D  A  L  G  E  E  Y  R

1836 CGGGGCCACGGCGCCGCCCGGCGATGTAGTCGTCGAGCCGGCGCCAGGATCTCGGCACAGCTTGCGCTGCACCTCGTCGAGGCGGCAGTT
     <R  A  V  A  R  R  G  A  I  Y  D  D  L  R  C  L  K  R  R  L  I  E  A  Q  V  E  D  L  R  C  N

1928 GTGCCCCGCGTCTCGACGACGTAGTAGACCTGTTCCATGCCGTAGTAGCGGTAGATAGAACGAGAAGAGCAGCGGGTGCGCCATCGTGCGCGGGTGA
     <H  G  P  T  E  V  V  Y  V  Q  E  M  G  Y  Y  R  L  R  R  L  R  E  D  I  V  A  D  A  T  V

2020 CCACGCCGCGCCGCCGTCCGCGCGCCTACGCCGTCCAGCCACCTTCGTCGCGCCAGCCCATCGTGCCGGCCAGCCGTCCG
     <V  G  G  G  D  G  Y  A  G  L  V  K  T  P  Y  F  S  F  A  A  A  D  G  M  T  G  A  L  R  G

2112 CCCGACGCGCGCCGTGCGCAGCTGCGCGACTGCCGCCAGTCCTCCAGGACCTTGAGGCGTGTTCCCGGGCCACCCGAGCCAGCGCA
     <G  R  R  A  G  H  S  Q  A  C  D  E  L  V  K  L  G  H  E  R  A  V  R  L  V  P  D  M  D  V  C
```

FIG.11A(2)

2204 CTGGCCGTAGAGGTGCACCGGCAGCAGCGCCTTCGTCCGGGGGGTGACCGCCTCGGCCAGCAGCTCGGTGTCCATCAGGTAGTCGTCGGCGC
<Q G Y L H V P L L A K T R P T V A E A L L E T D M L Y D D A R

2296 GGACGTCCACGAAGACCGGCGTCGCGCCGACGCGTCGGCGGCGAGCACCGTCGGCGCGCCGTGTTGGAGACGGTGACCTCGTCGCCC
<   V D V F V P T A G V A D I A L V T P A A T N S V T I V E D G

2388 GGCCCGACGTCGAGCGCCTGGAGTGCGAGCTTGATGGCGTTGGTGCCGTTGTCCACCGTGACGCCAGTGCGGCATGTCGTGATAGGCGGCGAA
<P G V D L A Q L A L K I A N T G N D V T C H P M D H Y A A F

2480 CTCCTGCTCGAAGCCGCGCACGCTCGGCCGGAGGATGAGGTTCCCGGACTGAGGCGTCTGCACGGCGTCGAGGAGGTCGTCCGTTCCT
<   E Q E F G R V S A G L I L N G S E F V T Q V A D L L D D R E K

2572 TCTCGTACTCCGGCAGGTAGCCCCACACTCGGATGGTCATCTTCGCCCTTCTACGGTCGCACGCTCAT   <· A S T R S R L A R V S M

2661 GTAGTCGTTGTCCGGTCGAGTCGAAGTGCCTGACCGCTCAGGTAGTCGACGGCGTCCACGTAGCTGTTAGGGCTGCATGAACCCGCCGGCCC
<   Y D N D R D L G L A Q G S L Y D V A D V Y S Y P Q M F G G A R

2753 GCACGTCGCGATAGAGCCGGGAGAGTGGGTGCCCGGCCGTGTAGGCGGAGGCCGCGACCAGGCCAGTCGTCCACCGCCGGGGCC
<   V D R Y L R S L P H G A T Y A L G G V L S L C D D V V A P A

2845 AGCTCGTTGACGCGGTCATCTTCGCGTACTGGAACGGGGTCATCATCGTCGCGGGTCGCTCGTCGGTCGCCCGGACAGGTCGACCGACGCCGC
<L E N V T M K A Y Q F P T M M R R G R E D P D G S L D V S A A

2937 GTCGGGCGTTGGTCAACGCCGCGACCGTGGTGCGTAGAGCGCGGTGTCCAGGCCCGGCGACCAGCGCCCGGCCACGGCCCGTG
<   D A N T L A A G V T T R L A Y L R T D L G A V L A R A G A R P

3029 GCTCGCCGCGCGCCCGCGCGAGAAACGACGCGCTGGGCGATGCGTCCCGGGCGTAGATGCGGCATGGTGATCGAGCTG
<   E G G R G A C F G V A I D R A A Q A I G A Y I G L M T I S S

3121 ACCGGTCTGCCCGGCCAGCACGCGGCCCGCCACCGGGCCGCTCAGCAGCTCGTCGGCCCGGACCGGGCACCGGTCGAAGAC
<V T Q G A L V A D R R A G V P G R E L L E D A R V P C R D F V

FIG.11A(3)

3213 CACCTCCAGCGTCCCCGAGGCACGCCATTCCCAGCCGTCCCAGTTGTCCAGCACCGTGAGCCCGGTGCGCGGTGCACGACCGGCACGG
     <V E L T G S A R M G L G D W N D L V T L G P A D R H V V P V A

3305 CGAGGAACACGAGCCGTCGTGTCGCGCGCTGGGCGTGCACGAGAAGTGGGTCGCGATGGGCGCCATGCTGACCAGCACCTTGCGCCCC
     < L F V S G D D D R R Q A H V F F H T A I P A M S V L V K R G

3397 GACAGCAGCCAGCCGCCGCGTCGGAATGCAGCTCGGTGACCACGCCGTCTTGAGCGCGCCAGACAGGCGGCCTCGCCCTC
     <S L L W G G A G D S H L E T V V G P A D K L A G C V A A E G E

3489 CGCCATGCCCCGCAGCAGCCGCTCCGCCATCGCGCGCGTCCGCCGTGCTGCCGTGCACTCGTAGGTGAGGGTGAGCCCCGGCTGAGCT
     <A M A R L L R E A M A R V P P T G H Q W E Y T L T L G R S L Q

3581 GCACGTGCCAGGCCAGCCGGTGGACGCGTCGGCCTCGACGCGCATCAGCGCGTCGCCACGTCGCTGTACAGCCGGGTCAACCCCAGGCCG
     < V H W A L A T S A D A E A L R M L A T A V D Y L R T L G L G

3673 CCCAGCTCGGCGGGAACGGTGGCGCCCATCAACCCGAGCTTCGGCAACTGCTTCGAACGCCTCCACGGGAAGGTGCCGGTGCGGTCCGGTG
     <G L E A P V T A G M L G L K A F Q E F A E V P F T G T R D R D

3765 GGCGGCCTCGCACTGATTCTCGGGATCACGCGGCAAGCAGGTCGACCACCGTGCGCCCCGCGGCGTGAGCGGCGGCGGAAGATCGCCG
     <A E A S I R P I V G A L L D V V T R G A P T L P A R L D A A

3857 CCACCCATCTCTCCTCGGTCAGATTAGACATCGCCTGTGCCGAACCTGTCGTCGCTATCAGGGTGCGCGGCGATCACC
     < V

3947 AATTGCTGGCTGATTGTCCACGACGATGCTCGACACAGGGATACCCAGAATAGGCGGCAACCCCTGTCGTGCGCCGGAGT
     <V K I L F I A G P T K S S L F G L A P L A I A A R M

4039 TCGCCAAGTCTAGTTGGATCACTCGAGCTTCCCCGCAGAAGCCGTGAACCATGGGCCAGCGGTTGAGCGTCGCTATATATTCGGCCGACACG
     >S G H E V V M A S T Q E V V P A T M S V G L P A F F P L A A L T

4131 TGCGGAGGACTCGTGAAGATACTGTTCATCGCAGGACCGACGAAGTCCAGCCTATTCGGCCTCGGCCCCACTGGCAATGCGCCGCCCGGATG
     >V K I L F I A G P T K S S L F G L A P L A I A A R M

4221 AGCGGGGCACGAGGTCGTGATGGCTTCCACGCAGGAGGTCGTACCGGCGACGATGTCCGTCGGCCTTCCCGCTGGCGGCGCTGAC
     >S G H E V V M A S T Q E V V P A T M S V G L P A F F P L A A L T

4313 CCTCGCCGAGCTCATGACCACGACCGGGCCGGCATCCCGGCGGACGCCGCCTTCGTCCCCTTCGTCGGCGGCCGGATGT
     >L A E L M T T D R A G D P L R I P A E D A A F V P F F V G R M

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4405  TCGGCCGGCTGGCGCTGGCGGCGATCAGCCTGGATCCGCTGCGCGACCTGGTCGGCGGCTGGCGCCCGGACCTGATCGTCGGCGGCCCGCACGCCTAC
      >F  G  R  L  A  A  I  S  L  D  P  L  R  D  L  V  G  G  W  R  P  D  L  I  V  G  G  P  H  A  Y

4497  GCCGCGGCCGATCCTGGCCACCGAACTTGGGGGTGCCTGCGTGGCGGCCACCGGTCACCGGCAACCGGTGGACGCGGAGGGCACCATCCCGGG
      >A  A  P  I  L  A  T  E  L  G  V  P  C  V  R  H  L  L  T  G  N  P  V  D  R  E  G  T  H  P  G

4589  GGTCGACGAGGAGCTGCGGCCAGGCTGGCCGCGCTCGGCCTGGCCCAGGTGCCGCCGTTCCACCTGGCCCTGGACATCTTCCCGGCCAGCA
      >V  D  E  E  L  R  P  E  L  A  A  L  G  L  A  Q  V  P  P  F  H  L  A  L  D  I  F  P  A  S

4681  CCCGGGATCGACGACGTCCCGCCGGCGCAGCCGGTGCGACCGGTGCTGCGGTGGATTCCGACCAACCAGCAGCAGCCGGTGGCGCCGTGGATGCTC
      >T  R  I  D  D  V  P  P  A  Q  P  V  R  P  L  R  W  I  P  T  N  Q  Q  Q  P  V  A  P  W  M  L

4773  TCGCGCGGCCGGCGCGTCGTCCTGGTCACCGCGCGGCAGTCTGGTCACCACCACCACAACTTCGACTTCCTGCACGGCCTGGCCGGCAC
      >S  R  G  P  R  R  V  L  V  T  A  G  S  L  V  T  T  H  N  F  D  F  L  H  G  L  A  G  T

4865  CCTGGCCGAGCAGGACGTCGAGGTCGTGGTCGCGGCGCCGCCGGAGGTGGGTCGCCTGCACGACGTGCCCGGTGTGCGGCACGCGCGGCT
      >L  A  E  Q  D  V  E  V  V  V  A  A  P  P  E  V  G  R  A  L  H  D  V  P  G  V  R  H  A  G

4957  GGGCTCCCGCTGGACGTTGGTGCTGCCCCACTGTGACCTGATCGTGCACCACTCCGGCACGATGACCGCGCTGAACGCGGGGGTG
      >W  L  P  L  D  V  V  L  P  H  C  D  L  I  V  H  H  S  G  T  M  T  A  L  N  A  G  V

5049  CCCCAGCTGATCGTGTGCCCGGAGGAGAGCCGGTTCATCGAGTGGGCGCGCAACCTGTCGACCCTGGGCGTGGCGCAGACCCTCGCGCCGGGCGA
      >P  Q  L  I  V  P  Q  E  S  R  F  I  E  W  A  R  N  L  S  T  L  G  V  A  Q  T  L  A  P  G  E

5141  GGACACGCCGGAGGCCGTGGGCAAGGTCGCGCGGCTGCTGCTGGAGGATCCGGTTCACGCCACCAGCGCCGCGATCGCCCGGGAGATCG
      >D  T  P  E  A  V  G  K  V  A  R  L  L  L  E  D  P  V  H  A  T  S  A  A  A  I  A  R  E  I

5233  CCGAGATGCCCGGCCCCACGGAGGTCGTGGGCCAGCTCACGGAGTTCGCGACCCGGGGGCTCACGTGCGCGTCCTCGTGACCGGCGGAGCC
      >A  E  M  P  G  P  T  E  V  V  G  Q  L  T  E  F  A  T  R  G  L  T  C  A  S  S  .

                                                                              >V  T  G  G  A

5324  GGGTTCATCGGCTCCCACCTCACGGACGCGCTGCTCGAACGCGGCGACAGCGTCACCGTGCTCGACGACCTGTCCACGGGCCGCCCGAGCC
      >G  F  I  G  S  H  L  T  D  A  L  L  E  R  G  D  S  V  T  V  L  D  D  L  S  T  G  R  P  E  R

5416  GCTGCCCGGCGGGGTGCCGCTGCACCACGGGTCGATCACGACGCGGGCCGGGTTGACCCGGTCAGTGTGCCCGAGCAGGTGTCATCT
      >L  P  A  G  V  P  L  H  H  G  S  I  T  D  R  A  G  L  T  R  L  A  E  Q  C  R  P  E  V  I
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FIG.11A(5)

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5508  GCCACCTGGCCGCCCAGGCGGACGTGCGCAACTCGGTGGCCGACGCCACCTCGGACACCGGGGTCAACGTGGTCGGCACCGTCAACGTCCTG
      >C  H  L  A  A  Q  A  D  V  R  N  S  V  A  D  A  T  S  D  T  G  V  N  V  V  G  T  V  N  V  L

5600  GAGGCCGCCCGGGCCATCGACGCCCGGGTGGTCTTCGCCTCCAGCGGCGGCGCCCTCTACGGCGAGGTCGACGAGCTGCCCTCCCCGAGGA
      >E  A  A  R  A  I  D  A  R  V  V  F  A  S  S  G  G  A  L  Y  G  E  V  D  E  L  P  S  P  E  D

5692  CGTCCGGCCGGCCGGGCGCCGTACGGGGCCGGCAAGTACTGCGCGGAGCAGTACCTGGCTCTACAACGGCTCGACCC
      >V  R  P  A  P  W  A  P  Y  G  A  A  K  Y  C  A  E  Q  Y  L  A  L  Y  N  R  L  Y  G  S  T

5784  ACGGCGGCTGCGGCTCGGCGGCAACGTGTACGGGCCACGCCAGGACCCGACCGGCGAGGCCGGGGTGTCTCGATCTTCTGCGGCTGCCTGGTG
      >H  A  A  L  R  L  G  N  V  Y  G  P  R  Q  D  P  T  G  E  A  G  V  V  S  I  F  C  G  C  L  V

5876  GCCGGGGCGCCGCCGACGGTGTTCGGCGACGGCGAGCAGACCCGGGACTACATCTACGTGGCCGACGTGGTGGAGGCGTTCCTGCTCGCGGT
      >A  G  R  R  P  T  V  F  G  D  G  E  Q  T  R  D  Y  I  Y  V  A  D  V  V  E  A  F  L  L  A  V

5968  CGGGCACGGTGGCCCCGGCCTGTGGAACATCGGCACCGGGACCTCCACCAGCATCCGCAAACTACTGGACCTGGTCGGCGCCACCGCCGGGC
      >G  H  G  G  P  G  L  W  N  I  G  T  G  T  S  T  S  I  R  K  L  L  D  L  V  G  R  T  A  G

6060  GCGGTCCCGGACCCCGCTTCGAGCCCCCGCTGGGCGAGCTGAAGCACTCCGCGCTGGAGGTGACCCGCGCGGCCAGAGCTGCGCTGG
      >R  V  P  D  P  R  F  E  P  P  R  L  G  E  L  K  H  S  A  L  E  V  T  R  A  A  R  E  L  R  W

6152  GCGGGCCCGAACGAGGGTCTCGCCGACGGCATCGCCAAGGTCTACAAGTGGGTCGAGGCCGACGAACCGGTCCGGGGGGAGCGATGACCCGCG
      >A  A  R  T  R  L  A  D  G  I  A  K  V  V  Y  K  W  V  E  A  D  E  P  V  R  G  E  R  .
                                                                         >M  T  R

6242  AGGGGGTCAACGCCGGGTTAGGGTCGGCCACCATCACGGTCGGCCACCAACGAGATCCGTTGGCTGGACCGCGCTCGGCTCGCTGCTCGCC
      >E  G  S  T  P  P  V  R  V  A  T  I  T  V  G  T  N  E  I  R  W  L  D  R  A  L  G  S  L  L  A

6334  AGCGACACGACCGGCTTCGAGCTGACGGTCTTCTACGTGGACAACGCCCTCGGCCGACGGGCGCCAGCGTCATGTCGGCGTTCCCGG
      >S  D  T  T  G  F  E  L  T  V  F  Y  V  V  D  N  A  S  A  D  G  S  V  A  H  V  M  S  A  F  P  G

6426  CGTCCGGGTCATCCGAAACCCCGCAATCTCGGCTTCACGGCGGCGAACAACGTCGGCGATGCGCCCTCGGCGGAGGCTTCGACCACA
      >V  R  V  I  R  N  P  R  N  L  G  F  T  G  A  N  N  V  G  M  R  A  A  L  A  R  G  F  D  H

6518  TCTTCCTGGTCAACCCGGACACCTGGACACCTGGACGGCCGCGGGGGCTGGTCCGCGGGGCTGGTCGAGTTCGCGCAGCGGTGGCCGCAGTACGGCGTCATC
      >I  F  L  V  N  P  D  T  W  T  P  P  G  L  V  R  G  L  V  E  F  A  Q  R  W  P  Q  Y  G  V  I
```

FIG.11A(6)

6610 GGCCCGGTTGCAGTACCGCTACGACCCGGCGTCGACCGAGTTGACCGACTTCAACGACTGGACGCAGGTCGCCCTCTACTGGGCGGAGCAGCA
> G P L Q Y R Y D P A S T E L T D F N D W T Q V A L Y L G E Q H

6702 CACCTTCGCCGGCGACCTGCTGGATCATCCCTCGCACGTCACGGCTACCGTCCGCGACCGCGCGCCGCGGACGCTGGAGCACGCGTACGTGC
> T F A G D L L D H P S H V T A T V R D R A P R T L E H A Y V

6794 AGGGCTCGGCGCTGTTCGTCCGGGCCGCCGTGCTACGCGAGGTCGGCCTGCTCGACGAGGTGTTCCACACTACGAGGAGGTCGACCTG
>Q G S A L F V R A A V L R E V G L L D E V F H T Y Y E E V D L

6886 TGCCGGCGGGGCCCGGTGGGCGGGCTGGGCGGGGTCCTCCTACTCGACCTCGGCATCCAGCACAAAGGGCGGTGGCACCGGCGGCGAGCGC
>C R R A R W A G W R V A L L L D L G I Q H K G G G T A A S A

6978 GTACAGCCGGATACACACATGCGCAACCGCTACTACTATCTGTGACCGATGTGGACTGACCCGCAAGGCCGTCGCCGCTCGCCGCCC
> Y S R I H M R R N R Y Y L L T D V D W P P A K A A R L A A

7070 GCTGGCTGTTCTCCGACGTCCGTGGGCGGGGCGTGACGGGTCGGAGGCGCGGGAGACCTTCGTGGCGCTCGGGGTGG
>R W L F S D V R G R G V T G R T S A G V G A R E T F V A L G W

7162 CTGGCCCGCCAGGCCCGGTGATCCGGGAACGTGTCGCGGGGCGGCACGGGCGTGCGGGCCAGGAGGGACGGGCGCGGGAGAGCG
>L A R Q A P V I R E R R R R H R L L R A R G T G V D R A R E R

7254 GAAGGAAACCGTGCGGGGGATGAGCAGGCCACGGATTCTCGTCGGCAGGCCAACTTCCACTGGCAGGCGGGTTCAGCCAGACCGTCGCCGCGT
> K E T V R G .
>M S R P R I L V A G N F H W Q A G F S Q T V A A

7345 ACGTGCGCGGGGCGGCCCGGGAGGCCGAGTGCGAGGTGCGGCTCTGCGGGCCGCTGTCCCGGGTCGTGGACGCCGAGACGCGCCACCTGCCGGTC
>Y V R A A R E A D C E V R L C G P L S R V D A E T A R H L P V

7437 GAGCCGGACCTTCCGCTGGGGCACCCACCTGGTGATCATGTTCGAGGCCAAGCAGTTCCTCACCGAGGCGCAACTGGACCTCGTCGAGGCGGTT
>E P D L R W G T H L V I M F E A K Q F L T E A Q L D L V E A F

7529 CCCCCGACAGCGCCCATCGTCGACTTCGACGGCCACTGGGGTGCCGAGGAGGGCGGGGACGGCGACAGCGCGTCGGGCCGGTACTCCG
> P R Q R R A I V D F D G H W G A E E G G D G D S A S G R Y S

7621 CGGAGAGTTGGCGGCGGTTGTACTCGACCCTGAGCGACCTGATCCTGCAACCCGGCTGGGTCCGCGGCCCGGTTCTTCAAG
>A E S W R R L Y S T L S D L I L Q P R L G P L P A G A R F F K

FIG.11A(7)

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7713  TGCTTCGGCCTGGCCGCAGCGCCGGTGCGCCACCCGCTGGAACTGGGCACCGGCGCGCAGTCGCGCCCGTACGACCTCCAGTACATCGGCAGCAA
      > C  F  G  L  A  A  P  V  R  H  P  L  E  L  G  T  G  A  Q  S  R  P  Y  D  L  Q  Y  I  G  S  N

7805  CTGGTGGCGGTGGGAGCCGATGACCGAGAGCGCGGCGGCCCGCGCTGCGCCGGTGTGTGCGGACGCTGGT
      > W  W  R  W  E  P  M  T  E  M  V  E  A  A  A  A  R  P  P  L  R  R  L  R  V  C  G  R  W

7897  GGGACGGGCGGCAGTTGCGCGGGCTTCGAGGAGGCGACGCTCAGCGAGCCGGGCTGGCTGCGGGCGCGCGGCGTGGAGGTGCATCCGCCCGTG
      > W  D  G  G  S  C  A  G  F  E  E  A  T  L  S  E  P  G  W  L  R  A  R  G  V  E  V  H  P  P  V

7989  CCGTTCGGCCACGTGGTCGAGCAGATGGGCCGGTCCCTGATCTCGCCTGGTCCTGGTGCGGCCGCTGGTCACCAGCACGGGCCTGTTGACCCC
      > P  F  G  H  V  V  E  Q  M  G  R  S  L  I  S  P  V  L  V  R  P  L  V  T  S  T  G  L  L  T  P

8081  CCGGATGTTCGAGACGCTGGCCTCGGGCAGCCTGCCGGTGCTCCCGGTCCCGGGCGAAGTTCCTCGCGGCTCTACGGCGACGAGGGCGAAC
      > R  M  F  E  T  L  A  S  G  S  L  P  V  L  P  V  A  A  K  F  L  A  P  V  Y  G  D  E  A  E

8173  ACCTGATGCTCGGCGACGACCCGGCCGGAACGCTGAGCCGGCTCTCGGCCGAGCACGAACGGTACGGACGACTGGTCGGTGAGATTCAGGAC
      > H  L  M  L  G  D  D  P  A  G  T  L  S  R  L  S  A  E  H  E  R  Y  G  R  L  V  G  E  I  Q  D

8265  CGGCTCCGCGTCGAGTACGGCTACCCTCGCGTCCTCGCGGGACCTGCTGCTCGATCTGCTGGCCTGAGGAATGAGGAGCAGATGACCCCCTG
      > R  L  R  V  E  Y  G  Y  P  R  V  L  R  D  L  L  L  D  L  L  A  .
                                                            > M  T  P  L

8354  CGGATCGCGGATGGTCAACATACGTTCCGGTTGCCGAGGACGAGCGCAGTGATCACGTGCCCGCGCAGGGGTACGGCGGGATCCAGTG
      > R  I  A  M  V  N  I  P  F  R  L  P  S  D  E  R  Q  W  I  T  V  P  P  Q  G  Y  G  G  I  Q  W

8446  GATCGGTGGCCAACAAGATCAAAGGGCCTGCTCGAACTCGGCCACGAGGTGTTCCTGCTCGGTGCCCGGGCCAGTCCGGCTACGGCATCCACGCC
      > I  V  A  N  K  I  K  G  L  L  E  L  G  H  E  V  F  L  L  G  A  P  G  S  P  R  T  H  P  R

8538  TGACCGGTGGTGCCGGGCGAGCCCGAGGACATCCGGGCATGGTTGAAGTCCGGTCCGGTTGGACGTCGTCAACGACTACAGCTGCGGCAAG
      > L  T  V  V  P  A  G  E  P  E  D  I  R  A  W  L  K  S  A  P  V  D  V  V  N  D  Y  S  C  G  K

8630  GTGGATCCGATCGAGCTGCCCCGGGGTCGGCCTGGTGGCCGGGCTGGTGGCGAGCCACCACATGACCACCCGCCCGTCCTATCCGGCCTGTGTACGC
      > V  D  P  I  E  L  P  P  G  V  G  L  V  A  S  H  H  M  T  T  R  P  S  Y  P  A  G  C  V  Y  A

8722  CTCGAAGGCGCAGCGGGAGCAGTGCGGCGGCGGCGGAGCGGGAGATGCGCCCGGCGTCATCCCGATCGGGGTGGATCCGTCGCTGTACCGCCCCGGCGACC
      > S  K  A  Q  R  E  Q  C  G  G  G  G  A  D  A  P  V  I  P  I  G  V  D  P  S  L  Y  R  P  G  D
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FIG.11A(8)

8814 GCAAGGACGACTTCCTGCTCTTCATGGGCCGGATCTCCCCGTTCAAGGGCGCGCTGGAGGCGGCCGCGTTCGCCCGGGCGCCGGCGCCGG
>R K D D F L L F M G R I S P F K G A L E A A A F A R A A G R R

8906 CTACTGATGGCCGGTCCGGCCTGGGAGCCGGAGTACCTGGACCGGGATCATGGGCGAGTACGGCGACCACGTCACCCTCGTCGGCGAGGTGGGG
>L L M A G P A W E P E Y L D R I M G E Y G D H V T L V G E V G

8998 GGGTCAGGAACGTATGGACCTGCTCGCCACGGCGGCCATCCTGGTGCTCTCCCAGCCGGTGCCCGGTGGGGCGGCACGTGGTGCG
>G Q E R M D L L A T A A I L V L S Q P V P G P W G G T W C

9090 AGCCGGGGTGCGACCGTGGTGTCCGAGGCGGCCAGCGGCCACCCCGGTGGTCGGCACGACAACGGGCTGCCTGGCGGAGATCGTGCCGGCC
>E P G A T V V S E A A A S G T P V V G T S N G C L A E I V P A

9182 GTCGGCGAGGTGGTGGGCTTCGGCACCGGCTTCGACGAGCGGGAGGCCCGAGCTGTGTCCCGAGCCGTGCTCCCCAGGCGCGGAA
>V G E V V G F G T G F D E R E A R A V L S R L P S P A Q A R K

9274 GGCCGCGCGATCCGGTGCTGCGGGGGCACGTGGGAGATCGCCCGGCGCTACGAGGCGGTGTACCGCGACGTGCTGGCCGGCGCTGGTCCTGA
>A A I R C W G H V E I A R R Y E A V Y R D V L A G A R W S .

9365 GCCGGCCCGGGCGGCGGCTACGGTCGCGACCGTAGGGGGGTGCCCGCCGGAAGCGCCGGTGTGTCGGCGGTCCGACACCGGCGCGCCCG
<. S R D H L W P R P E P D T V E V P Q S M F V L V Y A R

9457 GCCAGGTCAGCTCCGTCGTGCAGCCAGGTCGCGCGGTCTCGGGGTCACCTCGACCTCGGTCACCTCGGTCTCGACCAGGACGTACGCGCGG

9548 CGGCGGCTGGTCCGTTCGGCTCTCGGGGCCGGCGTAGTGCGGCGCAGGTCGTGCGCGCGCCTCGCCGCGGGCAGGCGCAGGCGACGCT
<R P Q D T E N P G A Y H P A R F D H M V A E G P R L P C A V S

9640 GTCCGTGTCGTCGACCTTCGTGCTCCGTCATCAGACCTTCGATGCGGTCGTTGATGTTGATGGTGCGGGAGCACCCCGGTCGCAGGC
<D T D D V E D T M L G E I R D D H N I H H H P L V G G R H L G

9732 CCGGCAGGTACTGGAGACAGCCGCTGGACACCGTCGCCGTCGCCTCGAGCGGGGTCCAGATGCTCAGGCGCGACCAGCGGGGTCCATG
<P L Y Q L C G S S V T A E D L P T W I S L G R R S W R P D M

9824 TACGCCCTCGTCCTGGTGCCAAGAGTGGGGACGGGCGGCTTGAGGATCGCGCGGATCGCGTGGCCGTAGAAGTCGAGTTCGTCTCCTCGGGGAT
<Y A E D Q H W P T P A G Y R P P K L I A H G Y F D L E D E P I

9916 GTCGGAGGAAAGCGGGAGGCGATGGCCGCGCATCGGCGGCGAAGTGCGCGGTCTCCACCAACTCCGGCCAGGTATTTCTCCGGCCGGACGATCTGCG
<D L F A S A I A R C R A F H A T E V L E P L Y K E P R V I Q P

FIG.11A(9)

10008 GGAGACGGGCAGGCGCGGGCCGTCGTCGCCACCGGCCGGCGATGTCCCGGTAGTCGCCGGTGTCGGGCGACGCGTGATCGGCGAAGAGCCGGTCG
      < L R A P A A D D G R G A I D R Y D G T D P S A H D A F L R D

10100 TAGGCGGCCCGGAGCGCCAGGCGACCTCGGCGTCGTCGGCGAGTCGTGGGGAGAGTCACGAAGCCATCGCGCGTAAGCCTCCAGCCGACGGTC
      <Y A A R L W A V E A D D A L Q P L T V F G D R R Y A E L R R D

10192 GACGACCTCCGCACCAACAGTCCCCAGGCCATTTGACCACCTCTCGGAATAGCCTGTCCGGCGAATAAACCATACGGTAGGAACAGCGCG
      < V V E A G V T G V A M

10282 GCGGATACGGCTCCCGAGCGGGGAAATAGGGATTCGACTAGTATTCGGTCCCGCCGCTGCCAGAACGGCACGCGCTCTCGATTGTCCATTCAT

10374 CCCCGTGCGAGACTCGCCTCGATGTCCTCGATGTGTCGGTGGGGGGGTTGGGATGACCGGGCACAGCCGTCGCGCTGGACGTCGGCGGGGT
      > M T G H S A V A L D V G G V

10465 CGTCTACTACGACGAGCCGTTCGAGCTGGCCTGGCTCCAGGACACCTTCGACCGCCTCCAGGCCACGGACCCGACGCTGGACCTGCGTGCGT
      > V Y Y D E P F E L A W L Q D T F D R L Q A T D P T L D L R A

10557 TTCTGGAGCACGTCGAGCGGTTCTACCACTACGGCGAGGGCGACCCAACCGGCACGGACCTGGCTCCACTCGGAGGCCGCGCTGAGCTGG
      >F L E H V E R F Y H Y G E G D P T G R T W L H S E A A A L S W

10649 TCGCGGGTCCGGCAGTCGTTCCTGGGGCGAGCTGGCCCAGGAGATTCCCGGTGCCGTTCGCGGTCACCAGGCTGGCCAGGAACTACCGTCGT
      > S R V R Q S W G E L A Q E I P G A V R A V T R L A R E L P V V

10741 GATCGTGCCAACCAGCCCCGAGTGCGCGAACGTACTGGCCCGGTGCCGGGAGGTGCTCCTCGACTCCCTCG
      > I V A N Q P P E C A D V L A R W Q V S Q V C R E V L L D S L

10833 TCGGGGGTGGCCAAGCCCGACCCGGCCCTGCTCGGGCTCGGTGCTCGGCTGGCGTTGCTGGTGGGGCAACGG
      >V G V A K P D P A L L G L A L R R L A I P P A E L L V V G N R

10925 ACGGATCACGACGTCCTGCCCGCTCGGGCTCGGTTGCCCGGTGGCGTTCGTGCTGCCCGATCGGGACGCGCGCCCGGGCGGTCCA
      > T D H D V L P A L G L G C P V A F V L P D D P A Y R R P P G V H

11017 TCCGGACCTGGTCCGGGTCTACACGGAGCTGCGAGGGCGTTCGGCCCACCCGCCGCCCGGGCGGTCCTGG
      > P D L V R V Y T E L R A F R T G S P P A D A R V T T V A S L

11109 CGGCCCTGGCCGACTCCCCGACGAGTGCCCACCCCGCGTTCGAAGCCGGCCACCGGCGACTTTGACGAAGGAGTGCGCAGTTGCGACGCC
      >A L A D S P L T S A T P R S N A G T G G L •

FIG.11A(10)

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11200  CCGCAGCGGTGGTCGGCGGCCACCGGCTTCATCGGCTCACGCCTGTCTCCCGCCTGGCCGAGGCCGGGCATCCGGTGGCGGCTTCAGCCG
11291  TGCCGCCCCACCCGTCGTCGACGGCGCCCGGCCCGGGGCTCCGGAGGCGCAGGTCGTCTACTTCCTGCCGCCGGCTGAGCCCGGCGC
11383  TGGCGGAGCAGCAACGGAACGGGTCGTCGGGAACGCGAGTTGTTGCTGGACGTGCTAAGTGCGCGGGGGTGGACCACCGGCCGGGTG
11475  TTCGTCCTGGCCAGTCGGGGGCGGTGTACACGCCAGCTGTGCGCCGCCTACCACGAGCCGGTCGGCCACCGGGCCGCTCGGCGTA
11567  CGGCCGGGCGAAGCTGCGGCTGGAACAGGAGCTGCTGCGCCACCGACCGGTGCTGGTGACCCGGTGAGCAACGTCTACGGTC
11659  CGGGGCAGCGGCCGACCCCCGGTACGGTCGGTGTCCTGTCACACTGGCTGGAGGCCACCGGCCGATCCGGCTCCTTCGGCGATCCG
11751  GCCGTGGTGCGGGGACTACGTACCGTCGACGACGTCACCGGAGGTCATCGGCGAGCGCCGGTGACGGGCGGGACCGGCT
11843  GCCCACGGGTCGTGAACGTCGGGCTCGGGGCCTGCCCCACCTCCCTGCCGAGTTGCTCGAGACGATGTCCACGGTCGTGAGCTGGAGG
11935  TCATCCGGACGTCCCGGCGCAGTTCGACCATCGGGGCAACGGGCTCCAGCGGCGGCGGATC
12027  AGCCTCCCCGACGGCGTCCCGACGTGCTGGGAGGCCGGTCCCAGTGCTGCACCGGGCGGGGGGGTTCCCGCCCGACGCTGCAGCCCGGC
       >  S  L  P  D  G  V  R  Q  C  W  E  A  V  L  T  R  A  G  G  P  G  G  S  P  A  R  P  S  A  R
                                                                              <  .  G  P

12118  TCGGGAGAGGCGTCTCGGGGGCGGGAGCCGGGATTCCGGGGGGCGTACGGTGCCGGTCCCATTCCTTGCCCAGGCCGGGCTGCCGGTCCGTCCGG
       >L  G  R  A  S  R  G  R  E  P  P  Q  P  R  P  S  Q  Q  F  V  A  Q  P  G  G  G  R  R  G  V  A
       <E  P  S  R  R  P  P  P  F  R  R  L  R  A  R  R  L  L  R  H  S  L  G  A  A  T  A  A  T  Y  G
                                                                                     junction marker

12210  GAGGGCCAGTGGCAGGGCGAGCCGGGATTCCGGGGGCGTACGGTGCCGGTCCCATTCCTTGCCCAGGCCGGGCTGCCGGTTCCGTCCGG
       >  E  G  Q  W  Q  G  E  P  G  F  R  G  R  T  V  P  P  F  L  A  Q  A  G  P  C  L  V  P  S  G
       <  L  A  L  P  L  A  L  R  S  E  P  A  T  R  H  R  D  W  E  K  R  L  G  A  R  A  Q  N  R  G  A

12302  CCTCGCACCGCCCCTGCCAGTACGCCCGCCGCAGCAGGTACCGGGGGGTCAGCGCCGGGTCGATGTCATGGGTGACC
       >  L  A  P  P  L  P  V  R  P  P  P  Q  Q  V  P  G  G  Q  P  A  R  V  D  V  M  G  D
       <  E  C  R  G  Q  W  Y  A  R  R  L  L  Y  R  P  T  L  R  G  P  D  I  D  H  T  V

12382  GCGTGGTCCGGGAGCAGTTGCTCGCGGGAGGGGCCTTCATGGGCGCTGATGAAGGAGGAGTGTCCTCC
       >R  V  R  E  Q  L  L  A  G  G  G  L  H  G  A  D  E  G  G  V  L
       <A  H  D  P  L  L  Q  E  R  A  G  A  A  K  M  A  S  I  F  S  T  D  E
```

FIG.11A(11)

12451 CCTGACTGGAGGTTGCCCCCGGTACGGGCTGAGGGCCAGGTCGAAATCCAACCCGTGGGCGGTGCGCGAAC
>P .
<G S Q L N G G T R S L A L D F D L G H A H A F

12520 GCGGAGTCCACCCCATGCACGCGCCCCAGATCTTGATGTTCCCTGGTCACGGTGCCAGCCAGGTGGAACTGGCCGGA
<A S D V G M C A G W I K I N G Q D R H W G V L H F Q G S
junction marker

12603 GGTGACGTACCACGGCAGACGCAGCCGCGGGGGGCGGGGTGCCGAGCCAGCCAGGTGCCGCCGACCACGTGCCGCCGGCTCTTGCGGACGGGCGTCGA
<T V Y W P L R L A P R A L R T G V V H A G D R L S K R V A D V

12695 CGGCAGCGGCGTCGAGCGCACGTCGTCGACGAACATCAGATGTTGTGGGCCGCAGCGGGGCGAGCATCGCGTTGCGGGAGGCCGACAGG
< A A A D L R V D D D V F M L H H H P W R A L M A N R S A S L

12787 CCATTGGTGGCACCGAGGATGCGCATGTGCCGCGGCGGCCGGACCTCCTCGGCGACCTCCTCGGCCGTGACGGGCCGGTCCAG
<G N T A G L I R M T G G A A R V E E A V E E A A T V P R D L

12879 CAGGACGTAGTACTCGTCGCCGGAGAGCTGGGCCATGTGCCGGTGTTCTGCGGCGAGGTGTTCCTGGCGGATCGCCACCA
< L V Y Y E D G S L Q A M N H A L H K R V N E V R F A C I A V V

12971 CCATCGGGTGGTCGGACGGATCGCGGCTGACCACGAGGCGTTGTTCGGCATCGTCCCTCGACCATGAGCGTTGTGGGGCCGGCGGGGGAGA
< M P H D S P D R S V V S A N N P M

13061 GGCGGGCCCACCGGATCGCGTCCGCGGCAGCGTGCCGCAGGCCCCGGCGCCGCCGCCCACGGACAGGTGGCGCACCGCCAGCGCGGCGGCCGTCCGG
13153 TGAGCGGCCGGGGGGGCGGAGCTCAGGCCGCTTCGTCCTTGCTCGCGCGCCCGCTTGCTGGCGGTCGGGCCAGGTGCCGCGCGGAGGATGCCCATCGGTACGCCTT
13245 CGCGGATCGAGCGGCCGCGGTTGGGCACTCGCAGGTTCTGCAACAGCTTGTCTGGGGCGATCGATGATGCGCGGTCCAGATCGGACAGTGAGAACTTGAGGTGGTCGTCTTCCGCT
13337 TGGCGGATATGCACCGTCGGTTCGCCTGCGGCGATGCTTTCGCTCGTTGGCTCGTTGTTGGCTCGTACGCGGCAGCGGCCAGAGTCGGGTGGACGAGTGGTGTGCTTCCGCT
13429 CCTTGATTGTGGGATCTGTTGGCTCGTACGCGGCAGCGGCCAGAGCGTCATCGCCCGGACGCATCGCCCCTGGGAGGTGCGGTGTGCTGCGGATGCCCCCGGCACG
13521 GGAAGACCGTCAGCGCGGGAAGGCCGGGGTGCCCGCCCACTCGTGCCCCACTCGTGCTCGGCTCGTGTGCTGCGGATGCCCCCGGCACG
13613 TAGCCCGCCTGACGGGCCTGTGCGGCTTGGGCTCCAACTTCGGCAACCATCGGTTCGCGCTGCACAGAACCAGCGGAGGAACATTGAGGTTTC
13705 GAAGCCCTTCGCTACTGTCGATCGACATCACTGGCGAAATGAAACCGGACCGGAAGCCGATAGTTACGGAAAGTGACAATCGGCTGGCC
13797 CTGTCGCTCGGCTGAACTCACCAATACGCCAAAAGCGTAGCCGGCCCACTGCGGAGCGTCCACCCCCGAGGATATCGCCAGGCTTCCATG

FIG.11A(12)

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13889  CAGAACTGGCAGGATCTTTCATCTCAGCCGCACCTGGGCGACAAAACCCTGCTCAAGACCATGAGTAAGCAGGCGCGGGAAATCCATGCAGT
13981  GACATGTGTCACTTTAGACAACCCAGCTCCAGCCCAGGCCCACCACCCTGACAAAAGGGGGCGGAATCGCCACCAGAGCGACACCAGCACATTC
14073  CTAGGGGATTCCTTAGTCTGGCGAGCGTCGATCCCCCACCCGTCAATCAATTGCCCAGATCAACCACTCCG
14165  CACCGTGAGCAGGCCGACCGTCGGCAATGCGAACGACAGTCCACCCGTCCGGTAGCCTCACCGCGCGCGGGGGCACGGGCCGGA
14257  CACCGTCCGGCGTCGTGATCAGCGGGGTGTGTCGCCGGCTGTGCGGGGGACCGGCATCGCGCGGGGACCCGGACGAAGATCTCCG
14349  GCGACCTGTCAGCCCTGCAAGCGGGACCGGACCGGCATCGCGCGGGACGGACCACCCGACGGTTCAGCGCGGGACGATCGGGAAGCCGACT
                                < · R R S R D P L R S

14440  CGCGGGCCTCGTCCCCAGAGCCCGCCACCGCATCCCGCAGCGATCGTCGGGGCGCCCGAGCAGGTCACGCGCCCGGGTCGACGC
                 < A E D W L G G V A D R L S R R P R W G L L D R A P G P D V R
14532  GGGCCCAGTCGACGACTCCACGCAGCGCGGGCGTATCCGGCCAACTCCACCACTCGGTCGGCCACCCGCTCACCTGATCAACATCTCCACG
                 < A W D V V E V S G P R D P L E V V E T P V G S V E I L M E V
14624  AGGGAGCGGACCGGAACGGGCCTCCCCCGCCCCACGCGCGATCCCACGCGGTGACGGACTCCCGGCCGACCACCACCGCCTCGGGCGAC
                 <L S R V P V A E G R G V G I V R G T V S E R T A S V V A E A V
14716  GTCCCGCACGTCGACGTAGTCCCGACGGACTGGCGGGTGGGCCAACGAGACAACTCCACCTGGCCCGCCGTCGACCAGCAGGCGAA
                 < D R V D V Y D R H A R L P S L E V R A S R D R G A A D V L R V
14808  CGACGACCCGCCCCAACAGGCTGTCGGTGGCCACGCCCGGACCCGAGCCGTTCGCGAACCGTCGGCCGTCCCGAGCCGGCCCGC
                 < V V R G L L S D P P V G P G V V N A L R L V T A D V S G A R
14900  GTCGCCGCGAGCCACAGGCCTGGGTGGCGGCCAGCTTCGCCCTGCGTACATGTCTCCGGGTGGGCACCGTGGGCGGGGGAGCCCC
                 <T A A L V A Q T A A L K A R G Y M S E P Q T P V T A G A P A G
14992  GGGTGGCTCCTGGAGCGGTTCCAGGACCGGAGCGGTCACCAGCGGCCAACGGGTGCGCTCCAGGCGGGTGACACTCCACG
                 < P P E Q V R E L V S G L H V L R P R C R T R E L A A T V S W T
15084  TCGGGATCGTGCAGCTCGACGCAGCTCGGCGGCAGCTCAGGTTCCACTTGCCGCCGGTGGCGTTGACCACCGGCTGCTCGGCGTCG
                 < P I T C S S P L E A D T L N W K G G T A N V V A D P Q E A D
```

FIG.11A(13)

15176 AACACGGGGCGGGGCCAGCGCGGCGGGGGGCTCCAGGGTGGGCGACGTCCAGCGCCCCGGCCCGGCCCGGTACGGCAGCCCGGACGGGGACGCGGGCGGGCCAA

<F V A A L A A P E L T A V D L A R A R Y P L G A S P V R R A L

15268 CACGAGGACGTCGTCGCCCCGGGGCGGCAAGCGGCGGGCGCTCACGTGACGCCCGACGAAGCCCGTACCACCGACGACCAGGCCGGCGC

<V L V D D G R A A L A A S V H R G V F G T G G V V V R R A G

15360 CCATCCGTACCTCCTGGGGATCAGTCTGTGCGGCGGCGTCCAGGCGACCCTGACACAGGTCACGGGGCGCGCAACAC

<M   < ·   D R A G A A D L R G G P G Q C T V P A R L V

15449 CCTGGCCCGGTCGCGGAACCTCGTCCACGAGCCCGGGGCGGGGATCGCTGCCGTCACCTCCTCCGCGGCTGACCGGCGGTGACGGCGCGGA

<R A R D R V E D L L R A R A R I A T V E E A P Q G A T V A R V

15541 CGAACTCTCGCATCGTGTTGACGAACTGGTCCTCGGCCCGGAAGGTCAGCTCCCGGTCTCGCTGCTCCACCGCGCTCACCGGGTGC

<F E R M T N V F Q D E A P F T L E R T E D Q R E V R V V P H

15633 CAGGCCGGCGGGTGGGGTGTACGCCCGGTCGACCGGCTTCCCGGCGCTTCCCCAGAGCTGGTACTGCCACGGTAGGAGTGCTGCGAAACC

<W A P P P T Y A R D V V I R G A S G W L Q Y E C R Y S H E F G

15725 GAAGGCGGATCTGTGCGGGTCCGGCCGTACACAACGCGGCACCGGAAACGTCCACGCGGGCGATCGGGGTCTCCGGAGGGTGG

<F A I Q A T R G D P T C L L A A G S V D V G R D P D E R L T A

15817 CCGCCACCACCTCCGGCGCTCCTCCGGCAGGAAGAACCGGCCGCGCCCAACGGGTAGACGCGCCAGATCACAGCAGCGCTCCACCCGCCTCG

<A V V E P E E P L F F R A A G L P Y V G L D L L A G G G L E

15909 GGTCGGTAACGGATGTCGCCCGGCCCAGGCGGCGGAAACCCGGAAGACGCCGGAGACCATCGCCGGATCTCGCCGGCCGACCAT

<P R Y R I D G A P L P P F G F V G S V M R L E G I E G A A V M

16001 CCGGCGCACGAAGTGGTGCACCCCATGTCGGAGGAAGGTGAGGTTGTCCATCAACACGAGCCCACGGCCTGGGTCAGCTGGTCAGCACCGCCG

<R R V F H H V G H R L F T L N D M L V L G R S R A Q T L V A A

16093 CGGTGTGTCGACCCCGGGTGGTCAGCGGCTTCTCCACCAGCACGTGTTGCCCGGCCAGGGGCGCGGTTCGATCCCAGGTGTGTGCAGCCCG

<T D V L R T T L P K E V L V H K G A A L A R E I W T H H L G

16185 GTCGGCAGCGGGAATGTAGACGGCATCGATGTCCGGGGCGGTTCAGCGGCGGGCGCGGTAGCCCTGGGGCGCGGCGGCACCGGAACTCCGCGGCGAA

<T P L P I Y V A D I D P R D L V S Q Y G E A A A C G F E A A F

FIG.11A(14)

```
16277  GGCGCGCGCCTTGGCCAGTTCCCGCGCGCGGACCACCAGGAGCTCCGCCTCCGGGACCCGCCTGATCGCCGGCAGGGCACGGCGGCGGCGCGGCGGCGA
       <A  R  K  A  L  E  R  A  A  V  V  L  E  A  E  P  V  R  R  I  A  P  L  A  R  R  R  A  I

16369  TGTCGGGCGCAGCCGAGAACCCGATGCGGAACCGTCATCTCCGGACCGTCACCACAGGCTGCGGCAGGCAGGCAAGTGCGGGGCC
       <D  A  C  G  K  V  G  I  R  V  T  M  E  A  M  ·  <  W  L  S  R  L  C  A  L  L  S  R  A

16459  TCGATGTTGAGGTAGTAGCCGTGCCGGAGCAGGGCCTCCAGCAGCAGAACTCGTCCGGCACCTCGGTCGGGAAGTC
       <E  I  N  L  Y  Y  G  H  R  L  L  A  E  L  Q  R  V  T  V  W  C  F  E  D  P  V  E  T  P  F  D

16551  GTCGCCGGGCTGCGACCAGGAGGTAACGGTTCTCCGACCGGTAGAATCGCCCGCCTCCTCGGTGAGCACGGTGTCGTAGAGGACACGGTCGG
       <D  G  A  D  V  L  L  Y  R  N  E  S  R  Y  F  R  G  G  E  E  T  L  V  T  D  Y  L  V  R  E  P

16643  GGGCGGCTTCCAGCACCTCGGCCAGGAACAGTGGTCGGGGCCGGGCTGGTTGTCGGGATGCACTGCACCGTTGGGCCCATCTCCATCGCG
       <A  A  E  L  V  E  A  L  F  L  P  R  P  G  P  Q  N  D  P  I  C  Q  V  T  P  G  M  E  M  A

16735  TCGAGCAGCCCGCCTGGTAGCGCCGGTGCCACCAGGTGCGCCACTCCGTCGATTTCCTTGACCAGGAAGGCGACCACGCCCCGGTGCCG
       <D  L  L  G  A  Q  Y  R  A  H  V  L  L  H  A  V  G  D  I  E  K  V  L  G  A  V  V  G  R  H  R

16827  CGGATACAACAGCGGCTGACTCCACCCGGTCACCTCGCGGTTGTCGTTGTGCGATGCCACCGTGACGCCGACCACGAGGAGTGCGGCCGTGTCCC
       <P  Y  L  L  P  Q  S  W  G  T  V  E  R  N  D  I  R  V  T  V  G  V  V  S  F  H  R  G  D  D  R

16919  GCGCGGATCCCGTCCGGGTGTGCCCAGTGTGCCGGCAGCCCTCGTAGGCGGCCGCAGCGTCATCGTGCGGCCCTTGGCCCGGGTG
       <A  I  G  D  A  T  H  R  W  D  P  L  G  R  L  P  V  R  R  V  T  M  E  H  R  G  K  A  G  T

17011  AACCAGCTCAACACCGACCAGGTCGTGGATCACCGACAGGCCGGGGGCGCGGGGCCCGGCGGCGCCAGGTGCTCGTGGATCACCGACAGGCCGAGCGGCCTC
       <F  W  S  L  V  S  V  L  D  H  R  G  P  A  G  A  A  S  R  V  I  A  A  V  A  P  S  S  P  A  E

17103  GGTCTCCTGGGCCGCGGGGCCGTAGAAGGCGAGGGCAGACATGACAGCGTAGCGTGGCTCATGTTGACCAGCGGGCGGGCGTCCACCGCAGCGCC
       <T  E  Q  A  A  A  Y  F  A  S  P  L  C  S  L  V  T  R  T  D  M  N  V  L  G  D  V  R  L  L  A

17195  CGAGCAGTTGCGCGACCCTGCTCCGGACGTGGTAGTCGCCGGGGAGCCACCATGTTCCGGTTGCGGCTTGCGC
       <L  L  E  R  L  P  L  W  R  H  Y  D  G  A  P  V  D  E  D  V  Q  V  V  M  N  R  N  R  K  R

17287  AGGAACCAGGAGCCCTGCTCCGGACTGCAGGACGTCAACCAGCACCCGACCACGGCCCCCGGGCGGGGTGAAGTAGTCGAGGTACTTCGTGCCGCC
       <L  F  W  S  G  Q  E  S  Q  L  V  D  V  L  V  R  G  A  G  P  R  T  F  F  Y  D  L  Y  K  T  G  G
```

FIG.11A(15)

17379 GCCACGGTGCACCCGGGTGTAGTTGCTCCGGGTGGCCTGCCACCGTCGGCAGCCGGAGAGCTGCATGACGTTGATGTTGCCGGGCTCCACCTTGGCCT
       <G R H V R T Y N S R T A Q V T P S L Q M V N I N G P E V K A Q

17471 GGAGCAGGCAGTACGGTGTCCGTCGACGACCTTGACGAGGATGCCGAGGATGCCGATCTCCGGCTGGTTGATGATCGGCTGGTGCTGCCATTCG
       <L L C Y P T G D V V K V L M G L I G I E P Q N I I P Q H W E

17563 CGCACCGCGCCGTAGGTGGTCTGGACGTGCAGCGTCCCTCGATCACGAAGAACCGGCCGCTCTCGTGCCCGAGGTTGCCGGTCACGGGGTCGAA
       <R V A G Y T T Q V H L G E I V F F R G S E H G L N G T V P D F

17655 CGCCCACCCGGGCAGCCGGTCCAGCGACGCGGTCCACCGGCACCGGGTCCGGCGGTCGAACCAGGAGGAAGTCCGGCC
       <A W G P L R D L P V R D V E C Y T S R T R E A F W S L F D P R

17747 GGACCCCCTCGGGCGTGCAACGGCACCAGCCGACCCGCGCCGCCGGTCGCAGCAGCCACCAGCTCGGCGGGAAAAGGGTCGGTGGGAAGACCCGTCGTCCGCCAA
       <V G E A H L A S W S G G D V P G P R H P G A D R T L L P G D

17839 GCGCGGACCTTCGGGTCGGGCGACGAATCGCTCACCACAGCTCGGCGGGAAAAGGGTCGGTGGGAAGACCCGTCGTCCGCCAA
       <A R V K P D P S S S D S V

17930 CAGGCGGCAGATCGCTGTCGACCATCATGGCCGACCATCTCCTGAAGGAGACGGAGGGTTTCCAGCCGAGCCGTCTGGCGGGCCTTCGTCGGAT
       <. . W L E A L E A S F A H S S G D T D A L
       <L R L D S D V M M A V M E E F S V S P K W G L R Q R A K T P D

18022 CCGGCGCAGAGCAGCTCGACCTCGGGCGGGCCGGATGAGCGACTCGTCCACCACGTGGTCCCGCCAGTTGAGGCCCACGTGGGCGAAGGCC
       <A C L L E V E A P R I L S E D V V V H D R W N L G V H A F A

18114 GCCTCGACCAGCTCGGGGACGCTGTGCGGTGGACCCCGTCCCGGTGACCCGTCCCGGTAGTCCTCGGGCCAGCATCAGGACCATGCCCCG
       <A E V L E R V S H T V G T G L V Y D E P E D Q A L M L V M G R

18206 CACGTAGTCGCCCGGGGAAGCCCCAGTCCCGCTCGGCCAGGCAAGGTTGCCCAGGCAGGCTGCAATGCCCAGCTTCACCGCCGCCACGC
       <V Y D G A F G W D R E A S L N G L R L S S R I G L K V A A V G

18298 CCAGCGACACCTTGCGGGTGACGAACTCGGACGAGCTGGGCTGATTCGTGGTTGAACAGAATGCCGGAGACGGCATACATGCGTACGAC
       <L S V K R T V F E P G R V P S E H N F L I G S V A Y M G Y S

18390 TCACGGGTAGTTCTGCACCATGTAATGCCGAAGCCCTTGGCCGCCGAACGGGGTCAGTTCATTCTGGACGGGG
       <E R Y N Q V M Y H G F A K A A G Y P S R P H F P T L E N Q V P

FIG.11A(16)

18482 CTCCCGCACCTTGCCGAACATCTCCGACGAAGACGCCTGATAAAAGCGCGGCTGACCGGCTGCGGGACTGCGGGAATCCGACAGGCCCCCCA
      < E R V K G F M E S S S A Q Y F R P Q G A A P S R S D S L G G V

18574 CGATCCGCAAGGCTTCGAGATGGAGAGCACCACCATGGCGGAGCACCATCCTCCGCGTGGTGGACTTCGTGTTCGTGTGGACGCACGTACGAC
      < I R L A E L M R L V G M G T V E A T T S Q R W S V P V Y S

18666 AGCGGCGGCGAGGTTGTAGACCTCGTCGGCGCGCGTTCGATCGCCGCCACCAGGCTCGTCTGATCCAGAAGGTCGCCGCTGATCAGCTT
      < L A G L N Y V E D P A A R E I A A V L S T Q D L L D G S I L K

18758 GACCGCTGGATCAGGTTGCCGAAGGCTGCGGACCGAGGGCGCGGTCTGCCCGGCACCAAATACCTCGTATCCGGACTGAAGCAGGT
      < V A P D P Q R L S R V S P A T Q G R V L G F V E Y G S Q L L H

18850 GCTCCCGGAGATACGTGCCGTCTGCCGGTAATTCCAGTGATCAGCGCCGCCGTGTCAGGGTAGTCTCCAGCTGTGAAGCCACCTGGCC
      < E A L Y T G D Q G T I G T I L A R R T L T T E L R S A V

18941 GAGGCGTGACCTCGCGCGATGGCGGACCAAAGATCCGCCGTTCGAAATGGGGTCGGATCTCCCGCTCACGGTACGCGGAATCT
      > M V A L V A V M I

19033 CCAAGCGGATTCAGCGACCCGGAAAGCAATATAGGGAGGTTACTAGTAGTACTTTCCGGCCGGCAGGACGCCGGCCCGGACCGGCA

19125 GGATCGCCCGGTTCGGCGGCGGACCCATCCCGGACACCTTCACCGGAAGCTCTTCACGGCCGGATCGTCGCCGATGGCAAGCTGCTTGACTCC

19217 ACCGTTTGTCCCTAACGTCGGCGGAGCTGCCAGCCGGCCGGCGGGTTCACGAAGGGCGCCAACTTCCGGTGGTCGCGGTGATGAT

19309 GGGCTCATGTCGCAGAGCCGGCCCCGGGCCCGGCAGCACCCCCAGCCCATCATGGCGCGGTCGGCGGAGTTGGGCGGCTCTCCT
      > M V A L V A V M I

19400 CCCGATGGTGCTGGCCACCCTCGACAACACCATCATCGGCACCGCCCTGCCCACCGTGGTCGGCGAGTTGGGCGGCCTCAGCACGCTCTCCT
      > P M V L A T L D N T I I G T A L P T V V G E L G G L S T L S

19492 GGGTGATCACCTCGTACACGCTGGCCACGCCGCCTCCACGCCGGTCTGGGCAAGCTGGCGGCGGACATGTACGGCGGCAAGGTGGTCTTCGTG
      > W V I T S Y T L A T A A S T P V W G K L A D M Y G G K V V F V

19584 GCCACGCTGGTCGTGTTCCTGGCCGGGTCGCTGCTGTCCGGCATGGCGCAGAGCATCACCCAGCTGACCGTCTTCCGGGCCGTGCACGGGCT
      > A T L V V F L A G S L L S G M A Q S I T Q L T V F R A V H G L

19676 CGGCGGCGGGGCCGGCCTGATGGTCTGCGCCTTCGCCATCATGGTGGAGGTTCTGCGCCCGGACCTGCCCAAGTACCAGGGCATCATGTCGG
      > G A G G L M V C A F A I M V E V L A G P D L P K Y Q G I M S

FIG.11A(17)

19768 CGACCATGGGCCTGACCATGGTGGCGGGCCCGCTCGTCGGCGGCCTGATCACCGATGAGCTCGGCTGGCGCTGGTGCTTCTACATCAACCTG
>A T M G L T M V A G P L V G G L I T D E L G W R W C F Y I N L

19860 CCGATCGGGGCGGTGCGCCTGCTCATCGTGGTGCTGATGATGCACCTGCCGCGCCACACCAAGGCCCGGCGCATCGATTACGCGGGGTGCTGC
>P I G A V A L L I V V L M M H L P R R H T K A R I D Y A G A A

19952 CCTGCTCACCGTGGTCAGTTCGTGCGTGCTGGTGACCACCTGGGGCGGCATCACCTACCCCTGGGGCGGTCTCCGATGATCCTGGGGGCTGG
>L L T V V S S C V L V T T W G G I T Y P W A S P M I L G L

20044 TCGCGCTCGGGGTGCTGACCTGCGCGCTCTTCGTGGTGGTGGTGGAGCGACGGGTGGCCGAGCCGTTGGTGCCCTGGCCATGTTCCGCAGCCTG
>V A L G V L T C A L F V V V E R R V A E P L V P L A M F R S L

20136 AACTTCACCCTGAGCACCCTCATCGCCTTCCTGGTCGGCTTCGCCCTCATCGCGGGGCTGACCTTCCTGGCCCTGTTCCAGGCGGTGCA
>N F T L S T L I A F L V G F A L I A G L T F L A L F Q Q A V Q

20228 GGGTGCCTCCGCGTCCGACTCCGGCCTGCTGCTGCCCCTGCTGTCCATGGCGGCGGTCAACGTGGTCGGGGGTCGCTGATGAGCG
>G A S A S D S G L L L P L L S M A A V N V V G G R L M S

20320 GCGGGGCGTTCTACCGGCTGCTGATGCTCGCCGGGCTGCGGCCCTGATGACCCTGAGCCTGCTGCTCTTCGCCCTGATGGACGTGGGCACCAGC
>G G R S Y R L L M L A G A A L M T L S L L L F A L M D V G T S

20412 CGGACGGTCACCGCGGATCCCCATGGTCGGGCTTCGGGGCTGGGCCTGCTCATGCAGACCAGCCTGATGGTGGCCTGAGCAGCGTGGA
>R T V T A I P M V G F G A G L G L L M Q T S L M V A L S S V E

20504 GATGAGGAACCTCGGGGTGGCCGCCTCCACGTCCTGTTCCGCACCATCGGTGGGGGCGGTGGGGGCGTCGGCGACGGTCTCGCTGTTCT
>M R N L G V A A S T S T L F R T I G G A V G A S A T V S L F

20596 CCGTGCGGGTGCAGTCGGCGCTGGCCGATCGGGGGGTCGCCGACGTGGCGGACGTGGCGGACGCGCGCCGGGCTG
>S V R V Q S A L A D R G V A D V A D L L G H S A R L D A A G L

20688 GCCCAACTCCCCGGCCGTCCGTGTCCACTTCATGCACGGCGTGGCCTTCCTGATGACCGTGCTGGCGGGGGCT
>A Q L P R A V R V H F M H A V A S G T R W A F L M T V L A G L

20780 GATCTGCGTCGCGGCGGCGTGGTTCCTGCGCCGGCGGGTCACCCCGTTGACGTCGGCACCGGTGGCCGGGGGCGCGCGCCGACGTCGCCGCGC
>I C V A A A W F L R R R V T P L T S A P V A P E P A R D V A A

20872 CCGCGCGCCAGCAGCGGCGGCGCGCCGAACTACTAGCGGGATTTCCTCGTTCCTCGGGATTCGTTCCTAGGGTTCCTCGTTGACTGACGGGATTAACA

>P A A S S G R A P N Y .

20963 TTCTTTTCGGCGATCCGGAATCCGTCCATTCCCGTCGTCTGGCGATGGTCGACGGGCCGGCCCGTGCCGAGCGGACAGACAGATTCTCGGAT

21055 TGGAGCTCGATGTCCAGCAAGGATCGTCATCGGTGGAGGTCCGGCTGGGCCGATCCACGGCGTGCTGCCGATCGGGGCTGTCG

>M S S K I L V I G G P A G S T A A A L L A R S G L S

21145 GTGACGCTCCTGGAAAAGGAGACGTTCCCGCGATACCACATCGGCAGTGCGATCGCGTCCTCGTGCCGCACCATCGTCGATTCGTTGGGCGGC

>V T L L E K E T F P R Y H I G E S I A S S C R T I V D F V G A

21237 TCTCGACGAGGTCGACTCGCGGGGGCTACCCGCAGAAGAACGGGGTCCTGCTGCGCTGGGGCAACGAGGACTGGGCCATCGACTGGGCCAAGA

>L D E V D S R G Y P Q K N G V L L R W G N E D W A I D W A K

21329 TCTTCGGTCCGGGCGTCCTGGCAGGTCGACGGGACGACTTCGACCACGTCCTGCTCAACAACGCCGGCAAGCAGGGCGCCAAGATC

>I F G P G V R S W Q V D R D D F D H V L L N N A G K Q G A K I

21421 ATCCAGGGCGCGGCCGTGTCCAAGCGGGTGTTGTTCGACGGTGAGCGGCCACCGCCGAGTGGTTCGACCCGGAGTCGGGGTGAGGTCCGCAC

>I Q G A A V K R V L F D G E R A T A A E W F D P E S G E V R T

21513 CATCGATTTCGACTACGTGGTCGGGGCTACTGGCCAGGGTGGCCTCGCTGCCGGAACTTCATCTCCCGGCGGGGATCAAGTCATCTCCCGGCCCGACGGC

>I D F D Y V V D A S G R A G L I P S Q H F K H R P T E T F

21605 AGAACGTGGCCATCTGGGGGCTACTGGCGGCCAGGGTGGCCTCGCTGCCGGAACTTCATCTCCCGGCGGGGATCAAGTCATCTCCCGCCCGACGGC

>K N V A I W G Y W Q G G S L L P N S P S G G I N V I S A P D G

21697 TGGTACTGGGTCATTCCGCTGCGCGGGGACCGGTACAGCATCGGCTTCGTCTGCCACCAGAGCCGCTTCCTGGAGCGGCGCAAGGAGCACGC

>W Y W V I P L R G D R Y S I G F V C H Q S R F L E R R K E H A

21789 CTCGCTGGAGGACATGCTCGCGCCACTGGTACAGGAGTCCCGACCGTGCGCGACGGGCTGACGGCGAACGGGACGTACCAGCCGGGCGTGCGGG

>S L E D M L A A L V Q E S P T V R G L T A N G T Y Q P G V R

21881 TGGAGCAGGACTTCTCTGTACATCTCCGACAGCAGCTTCTGCGGGGGCCCCGGCGGCTACTTCGCGGCGGGGGACTCCGCCTGCTTCCTGGACCCACTGCTG

>V E Q D F S Y I S D S F C G P G Y F A A G D S A C F L D P L L

FIG.11A(19)

21973 TCCACGGGGTGCACCTGGCCCTCTACAGGGCATGCTGCTCGGCCTCGGCCACCATCCACGGTGACGTCACCGAGGAGGAGGC
> S T G V H L A L Y S G M L A S A S I L A T I H G D V T E E E A

22065 GCGGGCGGTTCTACGAGTCCCTACCGCAACGCCTACCAGCGCCTGTTCACCCTGTTCGCGGCGTCTACCAGCAGGCCGGCAAGAGGG
> R A F Y E S L Y R N A Y Q R L F T L V A G V Y Q Q A G K R

22157 CATACTTCGGCCTGGCCGACGCGCTGGTGCACGACAGCGGCGAACCGGAGTACGAGAAGGTAGACGGGCCGGCCTTCGCCAGCTCGTC
> A Y F G L A D A L V H D S G E P E Y E K V D G A R A F A Q L V

22249 GCCGGCCTCGCCGACCTGGACGACGCGGCGGAGGGACGCCACGACAGCACCGGCGGCGGCAGCGGACAACTCCGTCCGGCA
> A G L A D L D D A A E G R H D S T A A A P A E Q D N S V R Q

22341 GCTCTTCCTGGCCGCCGAGGAGGCCCGGATGGCCGACAGGCCCGGTCAGCGAGGCGCCCAGGTCAGCGAGGCGCCCAAGCTCGACAGCC
> L F L A A E E A R R M A D A R T P S A P V S E A P G K L D S

22433 ACGACCTCTTCGACTCGGCAACCGGCCTCTACCTGGTCACCACCCCGCGACTGGGGATCCGGCGCAAGCCGGCCGACACGCAGGCGGCG
> H D L F D S A T G L Y L V T T P R L G I R R A K P A D T Q A A

22525 GCAGAGCAGTCTGCTGAGGTTCCACCCCTGGTGGCCCCGGACCGCGCGGGGCTGCTCAACCCTCCCACCAACATCCG
> A E Q S A .

22616 GCATCCGGTGCCGGCGGCTGAGCCCGGGCCGGAGACAGACGACA
> M S R S L R R D A Q A A Q A A P A

22708 GTTGCTCGCCCTCGGCAGCGGCGTGGCCGCCGGAGCACGCGTCATGTCACGCTCCCTCAGACGACGGCCCAGGTCAGCGAGGCGGCCACCGGC
> S P A N P H A G H A A P V P S R V S T T V V T P F T E P

22798 GTCGCCCGCCAACCGGCAACGGCCCGGGCTCGGGTGCCCAGCGGGTGCAGCGACGCACGCGGCCGCCCGTTCACCGGAGCCGA
> M P V P P R L T P V S R R D G I D V Y E I P I R P A Q V Q I L

22890 TGCCCGTCCCGGCGCGGGTGACCCGGGTCTCCCGCCGACGGGCATCGAGATCCCCATCCGGCCGGCCAGGTGCAGATCCTG
> P G L L T P A Y T Y A G S F V G P T I R A R T G R P V R I T Y

22982 CCCGGCCTGCTCACGCCCGCCTACACCTACGCCGGTTCCTTCGTCGGCCCCACCATCCGGGCCCGTGCGCGGATCACCTA
< P G L L T P A Y T Y A G S F V G P T I R A R T G R P V R I T Y

23074 CACCAACGGGCTCGACACCCACGCCAACGTGCACCTGCACGGCGGCCACGTGCCCGCCACCAGCGACGGTCACCCGATGGACCTGATCCCGC
> T N G L D T H A N V H L H G G H V P A T S D G H P M D L I P

FIG.11A(20)

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23166 CGGGCGGGCTCGAAGGTCTACGACTACCCGAACCTTCAGGCGGGCGGGCGACGCTCTGGTACCACGACCACCACCCACGCTCTACGAGGCCGACCAC
      >P  G  G  S  K  V  Y  D  Y  P  N  L  Q  R  G  A  T  L  W  Y  H  D  H  T  H  A  Y  E  A  D  H

23258 GTCTACCGGGGACTGCACGGCTTCTATCTGATCGACGACCCGGCAGAGCATCACCTGGCGCTGCCGGCAAGTACGACGTGCCGATCAT
      >V  Y  R  G  L  H  G  F  Y  L  I  D  D  P  A  E  H  H  L  R  L  P  A  G  K  Y  D  V  P  I  M

23350 GCTGCGCAACGCCCAGTTCGACGACTCCGGCGCCCTGGTCTTCGGCCACCCGGACGACCGGGTCACCATCCTGGCGAACGGCAAGGCCCAGC
      >L  R  N  A  Q  F  D  D  S  G  A  L  V  F  G  H  P  D  D  R  V  T  I  L  A  N  G  K  A  Q

23442 CCTACTTCGAGGTGGCCCCGCGCAGGTACCGGTTCCGGCTGCTGAACGCGGCGCTGAAGCACGTCTTCCGGCTCAACCTGGGCGGCGGGGAACCG
      >P  Y  F  E  V  A  P  R  R  Y  R  F  R  L  L  N  A  A  L  K  H  V  F  R  L  N  L  G  G  E  P

23534 CTCACCCGCATCGCCACGGACGGCGGGCTGCTGCCGGCCCCCACCAGTCACACCGAGCTGGCGCTCTCCTCCGGGGAGCGGGTCGAGATTGT
      >L  T  R  I  A  T  D  G  G  L  L  P  A  P  T  S  H  T  E  L  A  L  S  S  G  E  R  V  E  I  V

23626 GATCGACTTCGCCGAGCACGCAGGCGGGCCGGTGTACCTCTACGACGGGGACAACCCGATCCTGCGCTTCGACGTGTCGTCCCGGGCGG
      >I  D  F  A  E  H  A  G  G  G  P  V  Y  L  Y  D  G  D  N  P  I  L  R  F  D  V  S  S  R  A

23718 TCACCGACCCCAGCCGGGTTCCGGTCACCCTGCGCGCCCTGCCGCCGATGGGCACGCCCACCGTGGAGCGCACCGTGTCGATGAGCTTCGAC
      >V  T  D  P  S  R  V  P  V  T  L  R  A  L  P  P  M  G  T  P  T  V  E  R  T  V  S  M  S  F  D

23810 ATGTCGGCCCGCCCCATCGCGCTCATGGACGGCAAACCGTTCGACCCTCTCCGGGTGGACGTAGCAGGTCAAGCGGGGCAGCACCGAGAT
      >M  S  A  R  P  P  I  A  L  M  D  G  K  P  F  D  P  L  R  V  D  V  D  Q  V  K  R  G  S  T  E  I

23902 CTGGAACGTGGTCAACGCGGATACCGATCCGTTCCCCTTCGACCATCCGTTCCACCTGGTGACGTTCCGGGTGCTGGGCCGCGACG
      >W  N  V  V  N  A  D  T  D  P  F  F  D  H  P  F  H  L  V  T  F  R  V  L  G  R  D

23994 GCGGGGCCGCCCCGGAGGACGCGGGCCTCAAGGACACGGTCTACGTGTCGCCCAAGGGGTCTGTGTCAAGATCCAGGTCACCTTCGCCACG
      >G  P  P  A  P  E  D  A  G  L  K  D  T  V  Y  V  S  P  K  G  S  V  K  I  Q  V  T  F  A  T

24086 CCGTACCTGGGGCAGTACGTCTACCACTGCCACTACCTGGAGCACTCGTCGCTGGGGATGATGGCCCAGCTGGAGGTTGTGCCCTGAGGGC
      >P  Y  L  G  Q  Y  V  Y  H  C  H  Y  L  E  H  S  S  L  G  M  M  A  Q  L  E  V  V  P  •

24177 TCAGCCGTGCAGGTCGACGATCGAGAGGGGTGGGCGCGAACAGGCTGCGCCACCCGAACCGGCGGCGGGGCCAGG
      <•  G  H  L  D  V  I  S  P  H  A  G  F  L  S  V  P  R  V  D  G  V  G  F  G  A  A  R  A  L
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FIG.11A(21)

24268 TCGGCCTGGTCGGCGAACTCGTGCAGCAGCAGTACCGCCCGCGCTGCGACGTCACCGGCGCAGCTCGCGGAAGAGGGCGGCCGGAATC
      <D A Q D A F E H L L L V A R G G D V T V R R L E A F L R G S D

24360 ACCGGGCGAGCACGCCCCGCCGCTGCACCTGCCGGTCCCAGGGCGGATTGCTGACCACCGGTCCACCCGACCGGTCCGCGCAGCGGCAATCGTC
      <G A L V G R A Q V Q R D W P P N S V V R D V R G T R L P L R G

24452 CGGGCGTCGGCGACCGCGCCCAGGTGACGCGGGCCCCGACGCGCCGCCGAGTTGGCGACGGCGTCTCCGGGTCGTGGTCCGAGCCG
      <A D A V A W T V R A G S A A S N A V A A G V T E P D H D S G

24544 AACAGCACCGCCCCGGTGCCCCGGTGCCAGCCCGCTGCCTCCACGGGGATCGGCGCTGTGCCGGTGCCGCCAGCAGGCCACCGGGGCGGAT
      <F L V A G P A L G A A E V P I T G C C P D A V L M G P R I

24636 GCCGGCCAGCCAGGCAGCGCCGGGGCGCGGCGGGGGAGCGGCGGTGAGCGGCGCGGTGCCGGTGCAGCGGCCGGT
      <G A L W A L A A A L P P H L T G P T S S R K Y A R R H L P R D

24728 CGGCCACCCGTACGGCCAGGCGTCGCCTGGGTGCCCTGACCGGTGACCGCGCCCACGCGCGG
      <A V R V A L T A Q T G E V T V R L S L G G E P P A E G G R R

24820 GAGTGGTAGCGCAACCCGGAGCGCGGGCACGCCGCCGCAGGCGGCGACGCCGCCCAGCC
      <S H Y R L G L A A V A H R G V A D E I D Y R N Y N R R G L F S

24912 GGCGGGCGACGTCCAGGTCGCCGCCTTGGTGTGGCCGACGCGGTGG
      <A A V D V T A P R G P V G C A A R A P L V A P L A A A R A L R

25004 GGGTGAAGGCCGCCAGGTCCGCCTTGGTGTGGCCGGGGAGAACCACACCTGGCACGGTC
      <T F A A L D A K T H G V G D A V A V L L F L D D V T R L D L

25096 AGGGCGCGGCTCCGGCTGGGCGGGGAGCAAGCCCGCTCCTCGATCTCCTGGGC
      <L R P E A S A A S F W V E R H R H E V R G L G R E E I E Q A

25188 GGCCACCTCCTCCGCAGCCCTGCGCAGGGTCCGGTGCCATGAAGCGCACCGTCACCGTCCGCGATCCTCTCCCGCCCGGGTCGTCCCGCCGCC
      <A V E E L G R L T R A M

25278 GTGCCGGCGGCGTCCGCGAGCCTACCCACCGCACCGCGCGGACGCAGCCGACCCGCGCGGGGGAGCCGACGCCGA

25370 CCGGACCCGCCCAAGACTAGGTGAACCTCTATAGGAATTCGGTGCCCCTTCATAGGGTCCGAAAGGGGTAATGGAACCGTCGGGCACCGGA

FIG.11A(22)

25462 CGGCTCGTTTCTTCCCCAATTCCGTCGTCCGACCTGAGCCGTCGCAGGGAAGGCGAGGCCGAGCAGTTGATCGGTCGATG
                                        > M

25553 CCGCACGGGCCCGTGCGCCGAAATCGTGGAGATTGCGCAGTGCTGCTACACCGGATCTGTTCATCGGCGCCCTTCGTCCCGCGGAC
  > P H G P V R N R G D C A V R T P D L F I G A V G A F V P P T

25645 GGTGAGCGTCGAGTGGGCGGATCGACCGCGGTCTTTACTCCCGCGAGCAGGTGAGCTGGAGCTGCACGAGCCATCGCCGGCGACC
  > V S V E W A I D R G L Y S R E Q V E L H E L A G T A I A G D

25737 TGCCCGCCGCGGAGATGGCGCTGCGCGCCAACAGGCGGTCAAGCGCTGGGGCGGCTCGCCGACGGAGTTCGACCTGCTGCTCTACGCC
  >L P A P E M A L R A A Q Q A V K R W G G S P T E F D L L L Y A

25829 AGCACCTGGCACCAGGGGCCCGACGGCTGGCCGCCGCACTCCTATCTCCAGCGGCACCTGGTCGGCGGCGACCTGCTGGCGCTGGAGATCCG
  > S T W H Q G P D G W P P H S Y L Q R H L V G G D L L A L E I R

25921 GCAGGGCTGCAACGGGATGTTCAGCGGCTTCGAGCTGGCCGCGAGCCACCTCCAGGCGCACCAGGCGCCCTGCTGGTCGCCG
  > Q G C N G M F S A F E L A A S H L Q A V P E R T S A L L V A

26013 CCGACAACTACGGCACCCCGATGGTCGACCGCTGGCGGATGGGCCCGGCTTCATCGGTGGCGATGCCGGCTCTCCTCACCAAG
  >A D N Y G T P M V D R W R M G P G F I G G D A G S A L I L T K

26105 CGACCCGGCTTCGGCGCGCTCCGCTCGGTCTGCACCAAGTCGGTCCCGGAGGCGGAACGCCTGCACCGGGGCGACGAGCCCGTTCCCCCC
  > R P G F A R L R S V C T K S V P E A E R L H R G D E P L F P P

26197 GAGGCGTCCTGACCGGCCGGGAGCTGAACTTCACCGCCCGGATCGACCAACAGTTCGCCGCCCGCAGCCCCGATCGCCATGGCGGACG
  > S V L T G R E L N F T A R I D Q Q F A A R S P A S I A M A D

26289 TCGGGGACCACATCGAGGAGGTCGTGGGCCGCGCCCTGGCCGAGGCGGAGATCGAGGTCGGCGACCTCGGCCTTCATGAACTTT
  >V G D H I E E V V G R A L A E A E I E V G D L A R V A F M N F

26381 TCCCGGGAGATCATGGAGCAGCGCTGCCTGGCCAACTGGGGCCTGCCCATGAGCCGGTCCACCTTCGACTTCGGCCGGGATCGGGGCACTG
  > S R E I M E Q R C L A N W G L P M S R S T F D F G R R I G H C

26473 CGGGGCGAGCGACCCCCTTGCTGGCCCTGGAACACCTGGCCAGGACGGGGGGGCCTCGGCCCGGCGGCGATCACCTGCTGACCCTCGGCACCGCGC
  > G A S D P L L A L E H L A R T G G L G P G D H L L T L G T A

FIG.11A(23)

26565 CGGGCGGTGGTGGTCGTGCGCGATCGTCCAGGTGATCGAGTCGCCGACGTGGCGGGAGTGACCCGCTGGACACCTGCGGCGGGCCCGCCA
>P G V V V S C A I V Q V I E S P T W R E .

26656 GCCCAGCAAACCGACAGCAGGGGATGATTGTGGAAGCAGAGAAGGACCGGTTGCGTCCGAGCGGTCGCCGTGGTGGTGGGGA
>V E A E K D R L R P V A S E A V A V V G

26746 TCGGCTGCCGGTTCCCGGGCGACGTCAACTCGCCCGACGAGTTCTGGGACCTTCTGGGACGGGTCGCAACACCACCGGGACGGTGCCGAG
>I G C R F P G D V N S P D E F W D L L T G G R N T T G T V P E

26838 GAGCGCTGGAGCGGCGGTACCGCGCGCGGGTCCGGCGTTCGAGTCCGGCTCGGCAGCTTCCTGGCCGACATCTC
>E R W S A Y R D L G P A F E S A L R S A T R A G N F L A D I S

26930 CGGCTTCGACGCGGACTTCTTCGGCATCTCCCCGCGCGAGGCCGAGCTGATGGACCCGCAGCAGGGTCATGCTGGAGGTGACCTGGCAGG
>G F D A D F F G I S P R E A E L M D P Q Q R L M L E V T W Q

27022 CGCTGGAGGACGCGCGGGATCCCGCCCGCACCCTGGCCGGCACCGACGTCTCGGCGTCTTCGCCGGCGTGTGCACCTACGACTACGGCGGCCAC
>A L E D A G I P P R T L A G T D V G V F A G V C T Y D Y G G H

27114 CAGTTGGAGGACCTGCCGCACATCGACGCCTGGACGGGCATCGGCGCCGCCAACCGGGTCTCCCACGTGCTGCGACCT
>Q L E D L P H I D A W T G I G A A T C A V A N R V S H V L D L

27206 GCGCGGGGCCGAGCCTGTCGTCGATGACACCGCCTGCTCGGCGTTGCACCTGCCGTTGCACCTGCCGGTGGGCGAGAGCA
>R G P S L S I D T A C S A S L V A L H L A A Q S L R L G E S

27298 CGGCTGGCCCTCGCCGGCGGGGGTCAACCTGATCGTCACGCCGGGCAGTCAGTCGATCACCCTCGGCTCGGCCGGTGCCCTGGCACCCGACGGGCGC
>T L A L A G G V N L I V T P G Q S I T L G S A G A L A P D G R

27390 AGCAAGTCCTTCGACGCCACGGCCGACGGCTACGGTCGTGGCGAGGGGTCGCCGTCCTCGTGTCTCAAGCTGCTCTCGGACGCGCAGCGGGGA
>S K S F D A T A D G Y G R G E G C G V L V K L L S D A Q R D

27482 CGGGGACCGGGTGCTGGCCGTGCTGCGGGGCAGCGCCGTCAACCAGGACGGCCGTAACGGGATCATGGCACCGTGCGGCCAGGCCCAGG
>G D R V L A V L R G S A V N Q D G R T N G I M A P C G Q A Q

27574 AGCACGTGATGGTCCGCGCCCTGCGCTCGGCCGGCATCGAGGCCGGCAGCGTCGACTACATCGAGGCGCACGGCACCGGCACCCCGCTCGGT
>E H V M V R A L R S A G I E A G S V D Y I E A H G T G T P L G

FIG.11A(24)

27666 GACCCGATGGAGGCCGCGGCGATCGGCTCGGTCTACGGGCAGGACCGCCCCGACGACGAGCCCTGCTGCCTCGGTTCGGTCAAGTCCAACAT
>D P M E A A A I G S V Y G Q D R P D D E P C L I G S V K S N I

27758 CGGCCACCTGGAGGGCGCGGGCGTCGCCGGGGTCATCAAGGCGGTCCTGGCGCTGAACCGGGCCGAGGTGCCACCCTGCTGGTCA
>G H L E G A A G V A G V I K A V L A L N R A E V P A T L L V

27850 CCGAGGTCAACCCGGACATCGAGTGGAAGCGGCTGCGGCTGCGGCTGGTCACCCGCAACCAGCCCTGGCCGGACCGGCCGGGGCCGCCGC
>T E V N P D I E W K R L R L R L V T R N Q P W P D R P G P R R

27942 GCCGGAGTCTCCGGCTTCGGCTACGGCGGCACCGTGGCGCACGTGGTCCTGGAACAGGCCCCGCCGGTCGCGCGAGCCCGGCGCCCGGCGCT
>A G V S G F G Y G G T V A H V V L E Q A P P V A E P A P A L

28034 GACCGGGCTGAGACGCTCGTGTTCCCGGATCTCCGCGGGCAGCGCCCACTCCCTTCGCGAGCGGGCCCGCGCCCTGGCCGGGATCGTCCCGGATGTCG
>T G E T L F P I S A G S A H S L R E R A R A L A G I V P D V

28126 ACCTCGCGCTCGGGCACCTGGCTCGGGGCGTTCGCACCCTGACCCGGCCGCGGTGGCCGCCGCCGGGACGACCTGGTC
>D L A L G H T L A R R S H L T H R A V A V A A G R D D L V

28218 GCGGCGGTTCGCGGCGCTCGCCGACGACAGGCCGCACGACAGGCCGCACGACGGTGCCGGAAGCCGGGGTGGGCCCGCACCGGTGGGTGTT
>A A F A A L A D D R P H D R V R T G S P V A E P P R T V V F

28310 CTCCGGGCACGGGGTCGCAGTGGACGGGCATGGGCGGGAACTGCTGGCCACGGAGCCCTTCGCGACGGCCATCGAGCAGAGA
>S G H G S Q W T G M G R E L L A T E P A F A D A I D R I E Q

28402 TCTTCCTCGACGAGATCGGTTTCTCACCCGCCAGGCAGATCCTGGACGGCGACTACGAGGCCGTCGACCGGACCAATGATCTTCGCG
>I F L D E I G F S P R Q A I L D G D Y E A V D R T Q T M I F A

28494 ATGCAGCTCGGGCTGGCCGAGATGTGGCGCGCGAGGGGAGTCGAGCCGGACGCGGTGATCGGCCACTCGGTCGGAGAGATCGCCGGCGGGT
>M Q L G L A E M R A R G V E P D A V I G H S V G E I A A A V

28586 GACCGCCGGCATCCTGACCGTGGCCGACGGCGCACGGCTGATCTGCCGTCGTTCCTGCTGCTGCGCGAGGTCGCCGGACAGGGCGCGATGG
>T A G I L T V A D G A R L I C R R S L L R E V A G Q G A M

28678 CCCTGGTGACGCTGCCCTTCGAGGAGGTCGCCGCGCGGCTCGCCGGCCGCGTGGACGTGGTCGCCGCGATCGCCTCCTCCCCTCGTGTCGACC
>A L V T L P F E E V A A R L A G R V D V V A A I A S S P S S T

FIG.11A(25)

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28770 GTGGTCTCCGGGGACCCGGCCGCGCTGGACGCGCTGGTCGCCGAGTGGACCGAGGAGGGCCTGGGCGTACGCCGGGTCGCCTCCGACGTGGC
      >V  V  S  G  D  P  A  A  L  D  A  L  V  A  E  W  T  E  E  G  L  G  V  R  R  V  A  S  D  V  A

28862 CTTCCACAGCCCGCACATGGATCCGCTGCTCGACCGGCTGCGCGCCGCGGTCGACTTCACCGCGCGCCCCCGGGTGCCGATCTACAGCA
      > F  H  S  P  H  M  D  P  L  L  D  R  L  R  A  A  V  D  F  T  A  R  P  R  V  P  I  Y  S

28954 CGGCGCTGGCCGACCCGCGGGCCCCGATCACCGCCGACGGCGAGTACTGGGCCGCAAATCTGCGCAACCCGGTCCGGCTCGCCGCAGCGGTG
      >T  A  L  A  D  P  R  A  P  I  T  A  D  G  E  Y  W  A  A  N  L  R  N  P  V  R  L  A  A  A  V

29046 GCCGCGCCGTCTCCGACGGACACCGGGCCTTCATCGAGGTCTCCCCGCACCCGGTGGTGACCCACTCGATCCACGAGACGCTGGCCGGAAG
      >A  A  A  V  S  D  G  H  R  A  F  I  E  V  S  P  H  P  V  V  T  H  S  I  H  E  T  L  A  G  S

29138 CCTCGACGACGAGGTCTTCGTCGGCGGCACCCTGCGCCGCGACACCCCGGAGGCGCAGGCCTTCCTGTCCAGCCGCGGCCACTGCC
      > L  D  D  E  V  F  V  G  G  T  L  R  R  D  T  P  E  A  Q  A  F  L  S  S  L  G  A  A  H  C

29230 ACGGGGTCGCGGGTCGACTGGGGCCGGGTGCATCCGTCCGGGCCTGGTCACCCTGCCGGGCTACCCCTGGCGGCACCGGAGTCACTGGCAC
      >H  G  V  A  V  D  W  G  R  V  H  P  S  G  P  L  V  T  L  P  G  Y  P  W  R  H  R  S  H  W  H

29322 TGGCCGACGGCGCCGGCCACGGGCGCCGGGGCCACGACCCCGCGCTCGCTGGCGGTCGACAACGTGGCGGGCAGCGACGT
      >W  P  T  A  A  A  T  G  R  G  H  D  P  A  S  H  T  L  L  G  A  V  D  N  V  A  G  S  D  V

29414 GCGGGGTGTGGCGCGCACTGACGACGCCAGCCGCTACCCGGGCAGCCACGCCCTCAACGGCGTGGAGATCGTTCCGGCGGCCGTGC
      > R  V  W  R  T  A  L  D  D  A  S  R  P  Y  P  G  S  H  A  L  N  G  V  E  I  V  P  A  A  V

29506 TGGTTGGAGACCCTCATGGCCGCCGGGGCGGGCGAGCGGCCGCCGCTGCTGACCGGCTTGTCGATGCGGTACCCGCTGATGACCGCGGGG
      >L  V  E  T  L  M  A  A  G  R  G  D  G  R  P  L  L  T  G  L  S  M  R  Y  P  L  M  T  A  G

29598 CTGCACGAGGTCCAGGTGGTGCGGGACGGTGCCGAGGTGCGGCTGGCGTCCCGTTCCGTCGACGGCGGAGGCCGACCCGAGCCGGGACTGGCT
      > L  H  E  V  Q  V  V  R  D  G  A  E  V  R  L  A  S  R  S  V  D  A  E  A  D  P  S  R  D  W  L

29690 GATCCACACCGACGCCACCGTGGCCGACGCCGACGCCACGGTGCTGGCCGCGCGGGCGCTGGCCGACCCGGACGACCACCGGATGGAACCGG
      > I  H  T  D  A  T  V  A  D  A  D  A  T  V  L  A  A  R  A  L  A  D  P  D  D  H  R  M  E  P

29782 GCGACCCGGGCTCCATCCACCGCCGCCTGGCGGAGGTCGGGGTGCCGTCGACGGGATTCGACTGGTCGGTGGAGGAGCTGCTCTCCGGGTAC
      >G  D  P  G  S  I  H  R  R  L  A  E  V  G  V  P  S  T  G  F  D  W  S  V  E  E  L  L  S  G  Y
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FIG.11A(26)

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29874 GGCGTGCTCCGCGGCGGGGTGCGCTCGGCGCGTCGGTGCGGGTGCGCTCCACCTGGGCGCCGGTGCTGGACGCCGGTCATGTCGGTGCGCCCGCGTCTTCCC
       > G  V  L  R  A  R  V  R  S  A  D  S  S  T  W  A  P  V  L  D  A  V  M  S  V  A  P  A  V  F  P

29966 CGGGGTGCCCGAGCTACGCATGGTGTACGTCGACGAGGTGCTGCTCACCGGCGAGCCGGAGGTGACGCTGATCGAGGTCGCCCTCG
       >  G  V  P  Q  L  R  M  V  V  Y  V  D  E  V  L  T  G  E  P  P  E  V  T  L  I  E  V  A  L

30058 ACCCAGACCGGCCGCCGGACACGGCGAACGCGCTGGTCGCGGATGCTCAGGGCCGGGTCGTGGCCAGCCTCCCGGGCCTGCGCTACCCGGTGATC
       >D  P  D  R  P  D  T  A  N  A  L  V  A  D  A  Q  G  R  V  V  A  S  L  P  G  L  R  Y  P  V  I

30150 GACCAGCCGGTCGCCCCGCGCCAGGACAGTTCCGGCGAGGTGGAGGAGGCGGTCTCCTTCGCCGGCCTGTCCGACGAGGAACTGCACGAGCG
       >D  Q  P  V  A  P  A  Q  D  S  S  G  E  V  E  E  A  V  S  F  A  G  L  S  D  E  E  L  H  E  R

30242 GGTGTTCGACGAGGTGCGGCGGCAGATCGCCGGCGAGATGCGACTGGACGCCGACGACCTGCATCCCCGCCGGCCGCTGGCCGAGCAGGGCC
       >  V  F  D  E  V  R  R  Q  I  A  G  E  M  R  L  D  A  D  D  L  H  P  R  R  P  L  A  E  Q  G

30334 TCGGACTCGGTGATGACGGTGGTGATCCGGCGCCGGCTGGAGAAGCGCACCGGGGAGCCTCTCCCCGACCGTCTTCTGGCAGCGGCCCACC
       >L  D  S  V  M  T  V  V  I  R  R  R  L  E  K  R  T  G  R  S  L  S  P  T  V  F  W  Q  R  P  T

30426 GTCGCCGCCATCGCCGACCACCTGGTCGAGCTGTTGAGCACCCCGCAGGAGTGAGGAGTGAGGATCCGGCGACAGGAGGCCCGTGCGTTCCGCA
       >  V  A  A  I  A  D  H  L  V  E  L  L  S  T  P  Q  E  .

30517 CGGGCCCCTCCTGCTGTCGTGACGGATCTTCAGGTGGCGGGGTGGCGGCCGCTCAGCCCGGGTCCACCGCAGGGGTGGCGGCCCACTCCAGGTGGCG
       ·  ·  G  P  R  Q  D  V  A  P  T  A  A  W  E  L  H  R

                                                        <  ·  G  P  R  Q  D  V  A  P  T  A  A  W  E  L  H  R

30608 GCTCTCCCGCAGGGTCTCCTGCGGCGTTCTGTTCGACCCGGCGCCGCCGCCGCCGACGATCGGCGGCGCCATGGCCGAGGTGACGACGGCGGA
       < S  E  R  L  T  E  E  A  N  Q  E  V  R  R  M  A  V  R  L  M  P  P  A  M  V  S  T  V  V  A  V

30700 CCAGCACCACGATGGTGTATGAGGGCGGTGTTCAGCAGCGGTGTTGTTCAGCACCCATCGCCGATGATGATCTCCAGGCACCGCGCGGCGGTTG
       <  L  V  V  I  T  Y  S  A  T  N  L  V  G  L  R  L  G  V  M  A  I  I  I  E  V  A  G  R  A  N

30792 AGCCCGGCGCCGAGGGGCGACGGCCCTCCCAGTGGCTCTGCCGGGCCAGCCAGTCTGCCACCCAGGTACGCGCGGTGTACTTGCCGAGCACGGCGGAG
       <L  G  A  G  L  A  V  G  E  W  H  S  Q  R  A  L  R  A  G  L  Y  A  G  T  Y  K  G  L  V  A  L

30884 CGCCAGGATCACCGCGCCGCGCCCGGCGTCGGCGGAGGGCACGCGAGGCACCTCCGGGTCGGCGGAGGGCACGCGAGATCGGGGG
       <A  L  I  V  A  G  A  A  L  V  E  P  D  A  L  A  R  L  D  V  R  L  G  A  S  A  L  F  I  P  A
```

FIG.11A(27)

30976 CGAGCACGGACAGCACCACCGTGCGCAGCGGTGCCAGCCGGGCGGCTCCCGTTGCCGGGAAGGCCGGCCGGCCGATCAGGAGACACCGCCACCAGCGCG
< L V S L V V T R L P A L R A P E G N G P L G I L V G A V L A

31068 CCGAAGATCGGCCTCCAGGCCCAGGCGGTGCGCCCCCGCCGAAGGCCGCACGATCACCACGGCGCTGGCGGCCCGCCGTCGGG
<G F I A E L G L A H A G A A F A L V I V V A V A S A A G G D P

31160 CTGGGCGGTTCGCCCCAGGCATGGCGCGCGGGTCACCGGCGCCGGCCACCGCGGTAGGCCACGAGGTAAAGCAGGGCGG
<Q A N A W R M A R R T V P R G V L V A V A L Y A V L Y L L A T

31252 TCACCACCTGCCCGGCGGTGAGGGTGCTCACCGCCACCGACGAGATGAGCGACAGGAACCAGGCCGCAGGTCCTCCAGCGACGCGCCGCA
< V V Q G A T L T S V A V S S I L S L L F W A A A D E L S A A

31344 GCCAGGATGATCTGCCCCAGGTCGCCGGTGCAGCAGGCGCATGTCGGTGAGCGTCTTCGCGATCACCGGCACGGCGCTGACCGCCATCGCCAC
<A L I I Q G V D R H L L R M D T L T K A I V P V A S V A M A V

31436 GCCGACGAACAGCGGCGAAGACAGTCCGCTCCTGCCCGGCGCGAGAAGCGCCGGCCAGCAGGCCGGCGATGCCCAGGCCGAGGG
<G V F L A F V T R E Q G A A L L A A P A L L G A A I G L G L P

31528 GCACCCGCGAGGCCGCCCAGGCCGCCACCGGCCGCCGATCGTGCCGCCCAGCGACAGCGGCCGCCCGCCAGGTCGCACGGCGACC
< V A L G G V A V A G I T G A R R V L R L D L H L G A V A V

31620 AGCAGTACGACGCCGAACTGACGATGGCGTCGAGCAGGTGGACCTGGTCGGGGGTCGGGGGACCTGGGGGTCGATGTGGGGTGCCAG
<L L V V G F Q G I A D L L H V Q D P D A P L L W R G I D P A L

31712 GGCCCCCAGCGCACCGGAGGGGCCGAGCAGCAGCACCCGGTCAGCAGTCAGCGCCCGCCAGCGTTGCGCCAGCAGGCCGGAAGCGTTCCCAGGA
<A G L V S P G L L V G T L L E G V V A P L G F R Q A V R G L V

31804 CGACGGGCGAGCAGCAGCAGCCGCCACCTGGAGCAGGAACAGCAGTGTGGAGCCACCGGCCACCGGGCGCGGCCACGATCA
< V A L L L L G V Q L L F L L L Q H S G L P P V

31894 CGGTCGTTGTTCCTTTCGTCTCGACGCCCGCCAGGTCGGCGCGGGCTTCTCCCAGCCCGGGCGGCGCTGGGGCCGCGATCTCGGGCGCCGAGT
< · A A I E P P L D V P D A S N

31985 TCATGAAGGTCCGCAGGCCCGCAGGTCGGCGGCGGGCCCGCGAGTCGGCGGACCAATCGATGAGGAGGTCAGCTCCCCGGTG
< M F T R L A R L D A A P K E W G L G A C W D I L S T L E G T

FIG.11A(28)

32077 GCCCGAACCTTGTCCTCCTGGGCAGGCAGGCTGAGCACCGACATCTCGGCGGCCACTGCACCACGTTGGCCAGGTCCAGGTCGAGCCCCTCGGC
<A R V K D E E P L S L V S M E A P W Q V V N A L D V D L G E A

32169 CCGGGCGAACTCCAGCAGGTCGCGCAGCCCCCAGACGTTGTCCCGGTGGCCGCACCTGGAGCCCAGAGGTTGACCTCGAGGGGCCCGGC
<R A F E L L D R L G W V N D R Q P A V Q L W L N V E S R A R R

32261 GGACGTTGCGCGATGAAGGTCTCCCACTTCGCGCCCTGCCGATCCGCTCGAACACCTCGCCGTAGCCGTCGCAGGAGGCGCCGATGCCGATG
<V N A I F T E W K A G Q R I R E F V E G Y G D C S A G I G I

32353 CTCTTGAAGTGCCGGAACCGGTCGAAGACCGGTCCGGCAACACGGTGAGGTTGGAGTTGTAGAGCACGTTGCCGGTTACCGT
<S K F H R F R D F V S E P L V T L N S N Y V V D V N G A N G T

32445 CTCCACCAGCAGGTCTGAGCAGGGCGAAGTGGCCCGGCTGCATGAACGGCTCCCCACCGGCGAAGTACAGCCCGGATGAGGTGGGCGTTCT
<E V L L D L L A F H G P Q M F P E G G A F Y L R R I L H A N E

32537 CGGGCAGGGTCTGCCACAGCTCGTCGTCGTCCCGGTAGGCGTCGATGACCGGCAGGCCGGCCGCTTCTTGGCGCCCAGCCCGAG
<R L T Q W L E D D D R Y A D I V A S S W A P R K K A G W G S

32629 CTGACCCGGGTACGCGCACATCACGCCACCGCCAGGTTGCAGGTTGCCGAACCGGCTGGGGTCGGGTCGGGGTCGGACAGCGCGCCGTGGTCCT
<S V P Y A C M V C R L N C T N G F R I D L F F P D E V T G D

32721 GGGCGCGGTGCGGCGCCAGCCGGTCGGGGTCGGGTCGGACAGCGCGCCGTGGTCCT
<P A T R A A L R D P D A I D R F R Q N I E Q R Y S L A G H D E

32813 CGCGGTGGTAGCAGTAGGAGCAGGCGTCGACCGCTCCCCGGCCAGCCGAGCGGGAACCTCCGGCT
<R H Y C Y S C A D V R E G A L M A L R T R R M

32904 CGGCCAGGCCCATCACCCGGCGGGGTTGTCCCGGGTAGGGGACCGGCGTAGCGGGAGCAGGCCGTCGTTGAGCAGGAACTCCGGCT

32996 CCTCCTCCTCGTACAGCTTGTTGTGGTACATGGAGTCGTCCACGCCGTAGAGACGCGCCGTAGAGATGGATC

33088 CAGGGCAGCACGCACACATGGTCGGGGACCGGGCTTCCGGGTCCGGGACCTTCAGTCATGAAAGTTGATCACCTCGGTGGTGGGGGCGTGTCATCCCGGTCG
<•   G P R

33179 GCCGACCGTCTCGACCCGGGGAGTCGGCAGCCGGAAAGATCAACCGGTGCCGCTGGCCAGCATCTCCGGGCGACGATCTCGTCCCGGAAGT
<G V T E V R R P L P F F I L R T G S A L M E A E R A V I E D R F H

FIG.11A(29)

33271 GCCAGGGCAGGACCAGGTAGTCCGGGCGGGCCGCCCGGACTCCTGCTGCTGATGATTTCGATGTCCGTGCCGAGGGTGCGCGCCC
< W P L V L Y Y D P R A A R S E Q E S I I E I D T G L T R A G

33363 ACCTTGTCCGGATTGCGCTCCGGGGCGTACCGGATGAGCTCGGTCTATGCCGCAGAACTGCAGAGGGTGTTGCCCTTCGTCGACGCGCC
<V K D P N R E A A Y R I L E R D I G C F Q L L T N G K T S A G

33455 GTAGACGTGCACCGTGCGGCCCTGGCCCCGCAGCTCGGCGCAGCGGCGCTCACCGTGCTGGCGCACCTGCTCGGCGAAGCGCT
<Y V H V T R G Q G R L E R L L A S V E D R H Q R V Q E A F R Q

33547 GGTACGGGGCGGTGCGCTGCCGTCGCCAGCCCCAGCTCCCGGTCGGCGAGTGCCTTGCGCCGGCGCCCACCTCACCGGCC
< Y P A D G D L G L A L E R D A L A K V S G D A R G G V E G A

33639 CGGGTGACCACGCAGCAGATCGAGCCGCCGTTCACCCGTTGAGGCTGGCACGGACGATCTCCAGGCCCGCCGCCAGAATGCGGCTCAG
<R T V V C C I S G G N V G N L S A R V I E L G A A G L I R S L

33731 CGTGGCCAGGCAGTAGTAGGACAGGTGCTCGTGGCAGATGCTGTCGTAGCCGGCATCGCGCGGCAGGTAGGCGACCTCGACCA
< T A L S Y Y S L H E H C I S D Y G A I E L M A P L Y A V E V V

33823 CCCAGACCCCGCCGGGCGGAGCAGCGCCTCGACCGGCTCCTCGACGTCGTAGAACATCGCGATCGAGGTGACC
< W V G G P A L L A E V Q R A F E V P D E V D Y F M A I S T V

33915 AGGTCGAAGCTGCCCGGTGCGGGACCAGCTCGGGGCTGGGGAAGAAGTCGCGGATCAGATTGAAGTCGTCGGCGGCGCT
<L D F S G A H P V L E P S P F F D R I L N F D D P A D D A A S

34007 GGAGGGGTCGATGCCCACCGCTGCCGTCGGTCGGTCAGCCAGCAGGTGCCGTCGTTGCAGCCGATGTCGAGCCACCTTGCCGGCCGCT
<S P D I G W R Q A D T L N G L L T G D N C G I D L V K G P R E

34009 CCCCCAACACCTGCCGCCGGTCCGACGCGTCCCACGAGATGCGGCGAGCATCGTGTCGTTGATCCGGAGCGGTACCAGTAGGTGTCGTAG
< G L V E V A A D V V D A L H R R M T D N I R S R Y W Y T D Y

34191 AGCAGCGCCCACCCGGCCAGGGTGTGCCGCAACTGCACCAGCCGCCACCAGCCGCGTTCCGGCACCGGGTCAGCTCCAGGGGGAA
<L L G G P L T H R L Q V L G C P D G G D R E A C R T L E L P F

34283 GCGCACCCTGGGCGGGGTCCGACACGCGGGTTCACGAAGCTGCCCTGTAGGTACTGGCACCGGAGGTCGAGGACGTCACGCAGGGGTCCCGC
<R V R P P D S V G P K V F S G Q L Y Q A G L D L V T R L T G G

FIG.11A(30)

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34375 CACACACCCGGCCAGGTGGTCCGCTCGACCACCTCCGACGCGCCAACTCCTCGCCGGCGCCGCCGCCAACTGGCTCACGTCAGGTCCTCCTCGT
        < C   V   R   C   T   T   R   E   V   V                                < .   T   R   R   T

34464 CTCGTGCCGGTGTGCGGGACCAGGCGCCCGTCGTGCGGTTTGCTGGCGACCAGCAGGATGTCCAGATAGAAGGGCTGGTCGGGGCCTCGC
        < E   H   R   A   P   G   A   G   D   H   P   K   S   A   V   L   L   I   D   L   Y   F   P   Q   D   P   G   E   S

34556 TGCGGGCCGAGATGCCGGAACGCCCGGTCGAGGTACTCGTCGAGGTCGCGCGGGCGGGCGTCCACCAGCCACAGGGGCGGCAGGGCCAGA
        < R   G   L   H   R   G   A   R   D   L   Y   E   D   L   A   R   P   R   L   R   D   V   L   W   L   A   R   L   A   L

34648 CCCACCGGGCCGCCCGGACGCGGCCAGCCGTGCCAGCAGTACCAGCGCAGCAGCAACAGGCCGGCGCCGCCAGGTCAGCTTGACGGT
        <G   V   P   G   G   S   P   W   G   H   E   R   G   Y   W   E   L   L   L   L   L   G   R   P   G   C   T   L   K   V   T

34740 GCGGTCGACGGTGAAGCCGGCCACTGGCCTGGCCGGGCCAGCCCGTCGGGCGGGCCCACGGTCCTGGCGCGCAGGTCCTCCCACA
        < R   D   V   T   F   G   A   W   E   A   Q   R   A   L   G   D   A   T   W   R   W   L   D   Q   G   G   H   E   E   W   V

34832 CCCCGTGGGGTGGAGAGCACCAGCCGGGCGCCGGCCAGCAGCCGGTACGGCGTCCCGCAGGTACGGCGTCGTGTTCGAGC
        < G   H   T   S   L   V   L   R   G   G   P   R   L   L   R   Y   A   E   R   L   Y   A   D   A   D   S   V   H   E   L

34924 ACCTGGGGTGGAGAGCTGCGGCGGTCTGCAACTGGCCGGGAGCGGAAACAGCCCGGTATGGCGGAGGTGCCGCGCCGTAGTCGGAGACTCACC
        <V   Q   T   S   L   V   G   D   F   T   G   D   P   V   P   C   R   G   D   R   D   L   A   H   D   A   P   L   S   E   G

35016 GCCCGGGATGTCTGGCGGTCTGCAACTCGGCGGAGCGGAACGGTGCCGGGCCGTAGTCGAGCCAGGGACTCCGTGG
        <G   P   I   D   A   T   Q   L   E   A   S   R   F   L   G   R   Y   P   S   T   G   A   G   Y   D   L   W   V   G   T   A

35108 CGTCCCGGACCGCCTCCGCCAGGCGCGCCAGGTCCAGGAAGTGGGCGTATGCCGGTGGGGGGCCGGGCTCGATCCGCTCCCGGAAC
        < D   R   V   A   E   A   L   A   D   R   L   D   L   F   H   A   Y   A   W   D   G   P   R   P   E   I   R   E   R   F

35200 CGTTCGGCCATCACCTCGTCCAGCGACCCGGTGGGGGCGTCCGGCGGTGCCGGCACCGGTCAGCAGGGACCAAGCCCGGGTACGGCCGCCAGC
        <R   E   A   M                             < .   W   R   W   Y   E   E   H   P   Y   R   M   T   T   P   E   P   L   G   E   W   R   R   L   S   A   A   P   R

35290 AGGGTCACCAACGCCAGTACTCCTCGTCGGGGTACCGCATGGTGGTCGGCTCCGGCAGGCCTCCGGCAGCCCTCCAGCGCCGCAGCGACGCGGCGGGGCCG

35381 GTACTCGGAAGGGCTGCTCGCGGTGCGGTGCTCCGGCCGCCAGCAGGAGAGCAGCAGTCGCACCTGCTTGAGCCGTGATGTACT
        <Y   E   F   P   Q   E   G   A   H   E   P   A   A   R   R   Q   A   L   C   S   L   L   V   Q   Q   K   L   G   I   Y   E
```

FIG.11A(31)

35473 CCGGCACGTGCGGGGCCGAGGTCAGCTCGACCTCGGGGGCCGGTACTCGAAGTAGATGACCCGGCCGCTTGCCGGTCACGCCGGCGCG
      < P V H P G L D L E V E A P R Y E G Y I V R R R K G T V A P A

35565 GGCGTGCAGCATCAGGATGTTGTGCAGCATCACGTCGCCCGGGTTCATCACCGCCGGCCCCGGTGGTCGTCCCACTCGGTGGCCGTTCAT
      <A H L M L I N H L M V D G P N M V A P V A G T T D W E T A N M

35657 CCGGGTGGTGGTCTCGTTCGCCCGGTCGGTGTCCCAGTAGTTCGACTGCGGGATGCAACGCAGTTGTCCTCCGGGGCCGGGTCAAGGT
      < R T T E N A R D T D W Y N S Q P I C W V C N D E P A P D L Y

35749 AGATGCCGACGTCGATCACCCGCGCCACCCGGTGATGCCGGTCTTCTCGGGTAGAGGCCGCGTGCCAGGGCAGCAGCCGGGGC
      < I G V D I V R G A G T I G V A N E P Y L G G D R H W P L R P

35841 GCCCCCGCTCGGTCTTGAAGACCATGTGTCCCAGGTGGGGATGGGGTTGGGGCCGACCAGGTCTCCATCGCCCGCAGCAGCAGGGGGTG
      <A G A E T K F V M S D W T P I L N P G V L D E M A R L L L P H

35933 GCCGGGCGAGCCGGGCGACCACCGGGGACTTGTGACCACCAGTACTCGACTCCGGGCTCGTGGCGGTTCCAGCGTCCAGA
      < G A L R A V V P S K D V V Y E I R V P A A D P E H P E L T W I

36025 TGGTGTGCGGTCATCGTCCGGCCCAGGCTTCGTGATCAGCTCGGGGTCGTCGGGGTCTGGGGTCCAGCAGC
      < T D T M T R T R W A E D I L E D A A A Q V S R L E D P D L L

36117 CCGCGCAGGATCAGCGCGGCCCTGCCGGCGGGTCAGGTGCTCCGGAAGCAGCCCGGTCTGTGGATGTGGCACTCGGGGACGGCCTG
      <G R L I L A G Q R R F A T L H E P L L G T E H I H C E P V A Q

36209 CTCGGTGCGGACGTCCACAGTCGCGCTCATGGTTCGGTTCCCTTCTGCCAGGGACGGTTCGTGCTGCCCGGAGCCCGGCCGCCGGGCCCG
      < E T R V D V T A S M

              < • P E T G K Q W A S P E H Q G S G G A P G P

36300 GGCTCGGTCGGTCGGCGACGAAGTACCAGTGGCTCCCGGACGTGCTCCCGGCGGCGTGCCGGTCCAGCGCGGCGAACCCGGCCGGCGCCCG
      < S P R D A V F Y W H E R L A D A F G A R D L A P Q G A R R G

36392 GGCAGGGTACGCGCAGCTCGTAACCCAGCTCGGTCACGAGCAGCAGGTCGGCGGCCGTACTCCCGCCGCTGGTGCCGTACTCCCGCATGGCCGTGGTCGCC
      <P L T R L E Y G L E T V L L A W L D A S T T G Y E R M A H D G

36484 GCCGTGCTCGAAGACGATCACCGGCCGGGGACAGCTCCACGGCCCAGGGCGAGCACTCGCCCGCCCTCGGTGTCCACCT
      <G H E F V I V P R W R R L L E V A G R L A L V E G G E T D V K

FIG.11A(32)

36576 TGACCAGGTGATCCGGCGGGTCACCGGGGACGGTCCAGGCGGGAGCACGTGTGTGACCGTCAGCTCCGCAGGGTCTCGTCGGGCGGGTCG
     < V L D I R R D G P L V D D L R V T D V T L E R L T E D P R D

36668 TAGGGACGCCGGCGGCGCAGCCCGCTGTAGCCGGGGTTGGAGACCACGTGGAGAAGCTGTCCGGCGGTGCGTCCGGCGGCGGCGGCCAC
     <Y P R R L G S Y G P N S V V H V F S D R G T R E A A A A A V

36760 CACCGTCAGCGGCCGGGGAAGTCCCGGCGCAGCCCCTGGCGTACGACGGCAGCGCCTGCCGGCCACGTGCCGGCGGGGGCGACCCGCA
     <V T V G P F D R R L G E A Y S P L A E V A V H R G R P A V R L

36852 GCAGGTGACGCAGGATGTCGCCGGCCCGATGTGTTCCGGTTCGCCGGTTCCGGTTCGCCAGATCTGCTGCAGATCAGCGCCACGGTGAGC
     < L H R L I D G A G A G I D V T N A D P E C I Q E I L A V T L

36944 TGGTCGTACCAGTCGTTCATCGACAGCGCGCCGGCCTCGTCGTGCGGGAAAGCTCAGTGGACATCGTCACGTCCTCGGTCCGGCACGCC
     < · H V D D R E E T R C A

     <Q D Y W D N M

37035 GGTCCGGCCCCGGAGCGGCCGACGCGCGGGGGGCGGGGTACGGACGCGGGTACGGACCAGGAGTTCCAGCTCCGGCAGCTCGATCTCCGGCAGCTCGATCTGGACAGCTCCAGGCCGCGGCGGCGCG
     <P G A G S G V A P A T R V L L E L E R L E I E S L E L G A A R

37127 GACGTTCTCGACGACTCCGGGGCACTGAGCGCCGAACACCGGCACCACCCCGGGTGGTGCAGGCCCAGGCCAGTGCCACCTGCG
     <V N E E V V G P S Q A G F V P V V G A P H H L A W A L A V Q A

37219 CGACGGTGTGCCCACGGTCGGCGGCGAAGGCGGCAGGCCGTCGACCACGTCGAGCAGTTGGGCGTAGTCCTCACCCCGGAAGGGCGTGCGAG
     < V T H G R E A A F A A L G D V V D L L Q A Y D E G R F A H S

37311 TAGGCCCGCCAGTCCTCGGGGGCGGAATGCCGGTCGCCGGTGCTGGTCGCCGTGGGCGAGCGGCGGAGCCGCCGCCAGCACCCC
     <Y A R W D E P A F A Q D R H L A G T L L G H A L A S G G L V G

37403 GACGCCGCGCCTCCTGGCGCGGGCAGCACCTCCTTCTCGGCACGTTGAACGGCAGGTTGAACGTTGAACGTTGGCCAGCAGCCCGG
     <V G A E Q C R P L V E K E A G R D L L N F P V Q V V D L L G T

37495 TCGGCACCAGTCCGGCCAGGTCGGGGACGGTCGGGCGGGATGGCGGGGAACCCGCGACCTCG
     < P V L E A L D G A T V N A F G V H R A L G E R V F G A L V E

37587 GCGGTCTCCCGGAGCGGGGACGGTCGGGCGGCCAGCAGGTCGGGCCAGGTCGGGGTCGCTGGCCAGGCTGGCCAGCAG
     <A T E A L P V T P D D P W H V S Y V V D V H D T G L Q R L S A L L

FIG.11A(33)

37679 CTCGTCCCGGAGGAACGCGGGGTGCTGCTGTTACGCACCGTCCGTCCGGGCGGGTCGAGCTTGTGCGTCGCACGCCGGGCGGGTCTCCAGCC
       < E D R L F A P D S N R V T R G P P D L K H R R V G P R T E L G

37771 CGGCGGCCGTGGCGGCCGATCACGATCTCGTCCGGTGCGCGGGCAACAGGTCGGCGCCCCGGGCGCCTCGGCGGGCGCCCGCCGGGCCCGCCG
       < G A T A I V I E D R H A P L L D A L G R A L A A E A A G G G

37863 TACGCCCCGGGAGAGGTGTCGAAAAGGGTGACGCCCAGGTCGAAGGCCCGGCCGGCCTGGTCCTGCACGCCTGGTTCGATCCCGGCCCACTGGCC
       < Y A R S T D F L T V G L D F A R R V A Q G P E I R R G W Q G

37955 GCCGAGCGCCCAGGTGCCCAGGCGACCGAGCGCCGAGACCACCAGCGCCTCACGCAGCGCTGCGCGCCGTCTCCGCCGGTG
       < G L A W T G L G L A S V L P G R E G I C R Q R V

38046 CCCCACCCACGCCCGTCGGCCGTCGGCGCCGTCACGCGCCGTCCCCGTCGCTGCGCAGCGGTCAGGAAACACCAGCGCGTGTGATTGATCATCT
       < • A A P E G D S R L T L F V V G D H N I M K

38137 TGTCGGTGACCGGCGTCAGCCCGGCCTCGGCGGCGATGCCGGTCATCAACTCCACGCCGTGCCAGTTCAGGAACCCTTGAACTCCACGGGG
       < D T V P T L G A E A A I G T M L E V G H W N L F G K F E V P

38229 TTCGGCGGTGGCGGTACCGCTCGGCGTAGGTGTGGAAGAAGCCGCGGCCGTGTGTCGCCGAGGTCCAGGAAGTTGAAGCAGACAGCCCGCCGGG
       < N A D R Y R E A Y T H F F G R T N D G L D L F N F C F L G G P

38321 CCGCAGGATCCGCCGGATCTGACGGAAGTAGAGGAAGACCTCGAAGACGTTGAGGTGGATGAACACGTTCAGGGAGGAACCCGGCGTCGAACG
       < R L I R R I Q R F Y L F V E F V N L H I F V N L S F G A D F A

38413 CGGCGGTCGGCAGCTTCTCCAGGAAGTCGTTCTCGATGTGGTGGTAGGAGACGTTCTCCCGGCCCTGCCAGGTGGCGCGCCTTGTGTGAGG
       < A T P L K E L F D N E I H H Y S V N E R G E C T A R A K D L

38505 AAGGATCGGCTGACGTCGGGCAGCGCGGAGCACAGGGCGCACCCGGTCGGCGGAGCCCGGCCCATGATGCCCTGCCCGATCTGCCGATCTCGAAGAT
       < F S R S V D A C L V A R V R D A L G A A M

38597 CTCCGATTCCGGGCCCGAGCCCGAGCTGCTCGACGACCAGGGCGACCTTGTCGACACGGTCCTGGAGTACTCCTCGCGGCGGTGGTAGCCGG
       < • P R R A F E A V D E P S L A G T D A L R A L L

38689 CGAGCTGCATCTGCATCTCCGGCGTGTTCCACTCCCAGACGTAGTTGAGGTCGCCGGTGCTCCGGAGCGGACAGCCCGGGGGGGGTCC

38781 TGCGCGGCGGCCGTCGTCGCCGCTCTTCGCGTCGTTCATCGCGGCCGAGACCTCACTCGGTCTCTGTCGGGGTCTCGCGGGCGGCGGCTGCG

38873 GAAAACTGGGCGGGGCGGGGTGTCACGGACGCGGGCGAACTCGGCGACGTCCTCGGGGGCTCCGGGGCTCCAGCCGCGCGGGGCCGGGCCAGGAG
       < • P R R A F E A V D E P S L A G T D A L R A L L

FIG. 11A(34)

```
38964  TTCGGCCACCTGGACGGGGTCGGCCCGGTGGTGACGGACTCCGCCATCCGGCTGCCGCCACCCGGAATCGGTGGTCGTGAGAGGACGGGAGC
        < E   A   V   Q   V   A   T   P   G   T   T   V   S   E   R   M   R   Q   A   A   V   R   F   R   H   D   Y   L   V   S   G

39056  CGAGGGCCTCGTCGACCTCCTCGCGGGAGACGGCCTTCGTCGCCGGCAGGGTCTTCGTCGCCGGGTCGAGCCGCCTGGGGTCGTAGATCAGG
        < L   A   E   D   V   E   E   R   S   A   K   L   G   P   L   T   K   T   A   G   Q   P   D   L   R   R   G   Y   I   L

39148  GCGGTCGTAGTTGAGCGGCCAGGCAACTGCGGCACGCCCATGGCAGCCGAGCCCGTTCATGTAGCAGTTGGCGCTGCCGTGGTGCACCAGCAAGTC
        < A   D   Y   N   L   A   L   S   L   Q   P   V   G   M   A   L   G   N   M   Y   C   N   A   S   G   H   H   V   L   L   D

39240  GCAGTCGCGGGAGGGATGAGCTCCAGGGGCAGGTCAGTTGCTGAGCACCCGCCAGCGCCCAGCGGCCCCTCCACTCGGAGGAGGAGGCGG
        < C   D   P   L   I   L   E   L   P   C   N   S   L   V   R   V   N   P   P   L   A   G   L   G   E   V   E   S   S   A   A

39332  CGGTGATCACGACCTCCACGCCCTGGGCGGCGGCGGCGCCGCCGCGAGCCGGTGCCGCGGCCACTGCGGCCGTGGCGGAG
        < T   I   V   V   E   V   G   R   Q   A   A   A   D   V   A   H   R   L   A   P   V   Q   A   G   F   V   G   T   A   S

39424  TTGCCCCACCACCAGCGAGACCCGCTTGCCCGGCCAGGGGTCCAGTGTCCTGGGAGCCGGTTGTAGGGCTGGTAGCGGAT
        <N   G   W   V   C   V   R   K   G   R   R   P   G   L   L   W   P   D   V   D   Q   S   G   N   Y   P   Q   Y   R   I

39516  CGGGATCCGCCAGCGCCGTCGCCCATCGGCGGCCCATCGGCGGCCCATCTGGTCGGCGGCTCCGATCTGGTGCCGCTCCCACTCGACGC
        < P   I   R   L   A   D   G   M   P   P   I   A   V   D   P   S   P   D   I   A   Y   R   I   Q   H   R   S   W   E   V   G

39608  CGTACTTGCGGAACTCGGTCACCGGGGTCGCCGGAGACCAGGTCGGAGCCGGTCTCGGTGTCGATGAACCCGGAGAAGTAG
        < Y   K   R   F   E   T   V   P   D   G   S   V   L   D   L   G   P   E   T   E   I   T   G   I   F   G   P   S   F   Y

39700  ACGCTGGGGATGTGGTGCAGCTCGGGGATGTGGTGCAGCTCCCTCCACGGCCATGATGTCGTGGACCACCAGGTCGGGCCGGTAGTGGGGCGGGTA
        <V   S   P   I   H   H   L   E   A   V   L   A   G   E   V   A   M   I   D   H   V   V   L   D   P   R   Y   H   A   A   Y

39792  GTCGACCGCGTTGTCGTAGCTGCGTGACCGCGGTGGACCGTGCCTTCCAGTAGTCGGCAGGTGTCGAAGTCGGCGAGCGAGT
        < D   V   A   N   D   Y   S   R   Q   V   A   T   V   T   R   K   W   Y   D   A   L   L   D   T   D   F   D   A   L   S   D

39884  CCATCGGCCGCCCGTGAAGGGGTTCAACGGCAGCGGTTGCTCCACCATGTGCTGCGGGGTGTGGACGTAGAGGGCCTGGTGGAAGCCCAGCCGG
        < M   P   R   G   T   F   P   N   L   P   L   P   Q   E   V   M   H   Q   P   T   Y   L   A   Q   V   Y   F   G   L   R

39976  GCGCTCTCCATCATGTCGGCTCCGTCGGTCGAGCAGACGGGCATCATGCCCCGGCCGGCGAACAGGGCGAC
        <A   S   E   M   M   D   P   G   D   L   V   S   V   P   M   M   G   A   A   A   V   G   R   V   Q   S   P   S   C   A   V
```

40068 CTTGACGTCGTGGCCGGCCGCCAGGGCCCAGCCGCCCAGTTGGACACGGTGAACAGAACCT
< K V D H G A A R L A W A L P V M C M Y H G A W N S V T F L V K

40160 TCATCGCAGCCTCTCTGCCTGTGCCGCCGGAGGGGTTGGGGTCGCGGCCAACTCCCGCGGGA
< . S T L V P L E R A P
< M

40250 TCGGCGAACTCGATCACGATGGTGCGCCCCACTGGTCGGAGGGGTTCGGCCCGGAGCCGGTTCGGC
<D A F E I V I T R R W Q D S P N P G S G H V L R V D H V I F D

40342 CCCCTCCTGGAGGGGACCACCGGGCACCCCGGCCGCGTGCGCGCCGTGACGGTCGACGCGCCACGC
<G E Q S P V P R P G A D R V A T V D A D D P L L H S G P V G

40434 CCTCCAGACAGCCGTTCTCCGGCCCGGCGGTGTCCAGGCAGATGCTGATGTTGCAGACCGTTCCGGTGC
< E L C G N E P G A T D L C I S I N C V A H P P V N V R D R H

40526 CACGGCACGCCGCCGGCCCCGCCGCCCAGTGCCGCTCCTTGAGCACGCAACGCGAAGGCGGTGGGCCAGCC
<W P V G A A R L P E K L V L A F A T P V V P T G L V D A A V A

40618 GGGGATCTCCGGCCGGTGCAGCAACTGCGCCCCTGCTTTTCGAGGTTGTGGATCCGGCCAGTCCGGCGCCCTCGA
< A I E P R H L L E G Q P W D Q K E L N H I R Y L V P E A G E V

40710 CCTCGTAGTTCCAGTAGTCGGGCGTTGGCCCGCGCGGGAACCGGTCGATCAGGTTCACCGGC
< E Y N W Y D A N A R A P G A F R D I L S V A G A K L Q A L V

40802 TCGGGGGTCGAGCGACCGGCACCCGACGTGCCGCGATCCGTCGCGCTGCGCGGGAACCGGCTGCCTGGTCATCG
< E P D L V P G V H A I G D S R F R S A V A E R E R S M T T M
< . R

40893 GAGGCTCACCCCTTCGGTCGGTCGGTGCCGTGCGGTGCGGCCGACGATGTGCACACCTCGGCGGCCGGCTCGTGCAGC
< L S V G E T P R R T G T R R G V A I I D C V E P S R R E H L

40984 ACCTCCACCTGCGGAAGCCGGCGTTGTGCAGGCGGCGAACAGGGACTCCGGTCGAGCGCAGCTGAGCGCTGGGGCCTG
<V E V E A F G A N H L A A F L S E R D L W R V D V S L G R A Q

41076 CGGCTCGGGGTGCTCCTCGGGGGACCTGTAGCCGTCGTGTAGCCTCGCCCAGGTGGTGGAGAGGT
< P E P H E E R V Q K V T Y G D I P Q L D G V G G W Y H T S L Y

FIG.11A(36)

41168 AGATTCCCGCGCGACGCCCGATGTCTTCAGCAGGTCCACGGCTCACGCACGTGGTAGAGCAGGCCCGCGCAGAGGACGGGCGTCGAAC
   < I G A V G A I D K L L T W P E R V H Y L L G A C L V A D F

41260 TCGCCCAGTCGGTGAAGTCGATCCGCTCGGCGACGCGCCAGCTGGTTGACTTCCATCACCAGCTCCGGCG
   <E G L E T F D I R E V D A V R L E V N T I G N V E M V L E A R

41352 GCGCAGGTTCTCCGGACGCCCTCCAGGGCAAGCACCGTCGTGCCGGGGTGCCGAGGGCAGGGCTGTCCGGTCCCAGTGCGCCGA
   < R L N E P R G E L A L V T T G P H R A L A L T D A G E L A G L

41444 GTTCGAGGAGATCCGCGCGGTCGGGAAACGCACCGAAGAACTTCCGGCGCCCGGTCGGCGGGACTCAGCTGCTCAGATAACGTGCTGGGAG
   < E L I R R A D P F A G F F K A A R D A P S Q S L L Y G H Q S

41536 CCCTCGGCGTAACGCACTCGTCGTGATCCATTCACCCACGGCTCGAGCGCGGGACGGGCGACGAATCTCTTCACGGTCCATGG
   <G E A Y R V G D H E F G N V

41627 GATCAAAGCCTAGCGATGCCATTGCGGTTGCGGACTAGTGTTTCATCATATTCAGCGGCTCGCGTGCTGAGCCTTTGCTGTTGACCAGCCG
   < • R S A T S L R E N V L R

41718 GGCCCATTCCGGAATCCGGTCCCCGCGGATCTCGAAGGAGACTGGAGTTCCGCCGCCCACCTGGCGGTGC
   <A W E P I R D G G I E I D F S S Q L E A P G A D A A W R A T R

41810 GGGCCAGTCCTCGGCCAGCGGGGTGTCCAGTCCGCCGAAGACGATCGGCCAGTCGGTTCGCCACCTCGTCC
   < A L G E A L P T D T W D G F V S R A L E T A T Y A T R V E D

41902 CGCGACGGGCAGGTGGGGATCGGATGTCTCCGGCACGCCGCCGGCCAGCTCCAGCTGGTTGTTGGTGCTGACGA
   <R S P L H A I P H E P V G A A S R V A Q A L E L V T N T S S S

41994 GCCCACGTTGAATGCCCGCCCCCACGCGTCTCGGCCGGCTGGTGGCTGAGCTGAACGGCGGGA
   <G V N F A R G W A A E T E A A R S V V N V V D G V Y T F A R V

42086 CCTGGCGCCGCCGTCGCCGTACACGGTGATCGGCTCGCCTCGCAGGATCTGGTTGAAGAAGATGGCGACCGGGTTGCGGTACGGGTCCCGCATG
   < Q G G D G Y V T I P E G R L I Q N F F I A V A N R Y P D R M

42178 TTCTGCCACTCCGCCTAGACGGTTGTGTCATGCGGAAGGCGGTGAAGGCAGCCCCTGGGTCCGCGCTCACCTCACTCCAGCTCGCGCTCGACCAG
   <N Q W E G Y V N H M R F A T F P L G Q T R M T V E L E R E V L

FIG.11A(37)

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42270 GTACTTGGCCAGGCCGTAGCTGTCCGCGGGGACGCGGGGACGACGGACTCGCCGTCTCGCCGTGGCCGTAGACCGCCCACGGAGGAGG
       <Y  K  A  L  G  Y  S  D  A  P  V  P  V  V  S  E  R  M  P  T  E  G  H  G  Y  V  A  V  S  S  A

42362 CGAAACAGAAGAACCGCACGGCCTACGCGGGGTACGCGGTTGATCAGATTTATGCTGCCATCACATTGGTCGCTAGTTGAGCTGCTTCACC
       <  F  C  F  F  R  V  G  T  R  L  S  A  N  I  L  N  I  S  G  M  V  N  T  G  Y  N  L  Q  K  V

42454 GAATGGCTGATCGCCTCCGCGCGAAGGGCAAAGTGGAAGACCCGCTCGAATCGGTTCTCGGCAACAGTGAATCGACGAGTCCACGTC
       <S  H  S  I  A  E  A  A  F  A  A  F  H  F  V  R  E  F  R  N  E  A  F  L  S  D  V  F  D  V  D

42546 GGTCACCGAACCGACGGCCAGGTCCACCCCGCCGAACCCGCTGCCGCCGGCTGCCGCCGGCTCGTCCCAGAACGCGGTGACCCGGTGCCCAT
       <T  V  S  G  V  A  L  D  V  G  A  P  V  R  Q  R  S  G  G  S  L  D  D  L  V  T  V  R  H  G  N

42638 TCCTGACCAATGACTCCACCAGTGCGAGCCGATCTGCGGCGCGCCCTTCGTCGGGCGGCAACACCGAACATCCGGGGCTCCTTCGTCAATA
       <  R  V  L  S  E  V  L  H  S  G  I  F  G  A  G  G  T  V  L  C  R  V  M

42728 GATCCGGCGAAAGGGGTTGACCGAGCGGGCGATCTGCGGGGCGCCCTTCGTCGGGCGGCAACACCGAGAGAAAGCTTCGCCTCAGGGCAC
                                                                            <  .  P  V

42819 CGGGCGACCGGCCTCGGCCTGCTTCTTCAGGCCGTACTCCCACCAGTCCCGGCCAGGCCGTCGGCGGAAGG
       <P  S  R  D  A  Q  K  K  L  P  E  W  D  R  H  T  R  Y  W  D  I  T  E  A  L  G  D  A  F  A

42911 CGACCTCGGGCCCGGTAGCCGAGCGCCCGCAGTTTCGCGTCGGCGGAGTAGCCGGGCCTTGCGGTCGTGCACCCGCTCGACC
       <  V  E  P  R  Y  G  L  A  R  L  K  A  D  T  L  S  Y  R  R  D  H  G  K  R  D  P  V  R  E  V

43003 CGGTCCCACCGGCCCCCAAGGCGTCCAGCAGCCGCCCGGAGCCGTGGACAGTCCAGCTCAGCTGGACAGCCGTGGTGGTAGACCTCGCC
       <R  D  W  G  A  G  L  A  D  L  L  R  G  T  L  E  M  N  S  L  E  A  T  G  A  I  H  Y  V  E  G

43095 GGGGACACCGGCGGCAGCGAGGTCGGCAAGGACGGTCTGGATGCCCGGCCAGTGGCCGCGTTCCGGCGACGTTCCCGGCGTACAGCG
       <  P  V  G  R  D  V  V  T  Q  I  G  R  C  H  D  T  V  H  I  W  D  R  V  N  G  G  D  G  Y  L  P

43187 GCACCCGTCGCCCGTTCAACAGCTCGGTGACGACAGCTCTTCTCCGGAAACTGGTACGGCCCGTAGTTGTTGCGCACCGGGGTG
       <  V  R  R  G  N  L  L  E  T  V  F  L  P  I  L  K  E  P  F  Q  Y  P  G  Y  N  N  G  C  R  T

43279 AGGCAGACCGGCAGCCCGTGGGGTGCGGGCCGGTAGGCCAGGGCGATCCAGGGGTACGGGGGAGTTCGGCGCCGCCCAG
       <L  C  V  P  L  G  H  T  R  A  Y  A  L  A  I  L  D  G  G  A  K  A  A  A  Y  P  S  N  P  A  L
```

FIG.11A(38)

43371 GGGGGTGTCCTCGGCCCAGGAACCCTCGTCGGTGCCGTAGACCTGGTCGGTGGAGACCTGGACCCCGGGGCGACCCGGCGTCGAGAC
      < P T D E A W S G E D I S G Y V E D T S V Q V V R A V G A D L C

43463 ACGGCCTGCATGAGCGGTCTGGACGCCCTGCACGTTGGTGCGGACGAACTCCGCGAGTCGGGCGATGGACCGGTCGCGCACGTCGGGCGGCCG
      < A Q M L T Q V G Q V N T R V F E A S D A I S R D V H S E A A

43555 AAGGTTGACCACCAGTCGTGCCGGGCAGCAGCCTCGGCCAGCACCTGCCCTGGCCAGACGCCGTGTCGCAGACGTCGCCCTGGACGAAGGTGATCCGGTCCTGGAC
      < F N V V V D H G P L V E A L L A T D C V D G Q V F T I R D Q V

43647 CGGTTCGAGAGGTTGGCGAGGTTGCCCGCGTACGTCACCTTGTCCAGCTTGTCCAGCCTGCCCGCGTGTCGGGGGTAGGCACGGTGGCCA
      < P E L N A L N G A Y T L K D L V T V R A Q A T D P Y A G T A L

43739 GGTCGCGGACGTACTGCGAGCCGATGAAACCGGACGCGCCGGTGACGCGACGCATCAGAACCCCACCGGACTTCGCTGTGAT
      < D R V Y Q S G I F G A G G T V L V R R M

                                              < . V G V R V E S H D

43828 CGCCGAGGACGAACCGGTGCGTCTTGGGCACCCGGGGGACCACCCGCGCCTCCGGCCGCCGATCATCGAGAACTCGATGCGGCCGATG
      < G L V F R H T K P V R P G P V R A E R G I M S F E I R G I

43920 CCCTCGATGTAGGCACGCGCAGCACGATGGAGTCGCATCTCGGTCTCCAGCAGGGTGCAGTCGCAGTCGATCGAGGTGTACGGGCCGAG
      <G E I Y A G R L V I S H E I E T E L L T C D C D I S T Y P G L

44012 GTAGGAGTTGGCGGATGATCGAGCCGGCTCGAGATCGAGCGGCCGCGCTGACGTCGGCGGCGCGCTGACGTCATCTCCAGCATGTCGGCG
      < Y S N R I I S G A G V V P G V I R S G S V D A G A S I V V P

44104 GGCCGATCAGTTCGGTGCGGTCGTGTCGACCTTGCCCTGCGACCAAAGGCTGACCGGTTCATCTCCAGCACCGGTGTGATCTC
      < G I L E T R D D V K G E V L P E V S G L V F R N M E L M D A

44916 AGGTTGCCGGTCGTCCTTCCAGTAGCCCGTGATCATGTGGAGTCGAGTGGCCGCGGTGGCCGCGTGGTGATCTC
      <L N G T D K W Y G T I M T S D V R H G R D I M W Q V A D T I E

44288 CAGCTCGTTGCGCAGGACGGCTTCAGCTGCCCATCGTGGACCACCGGGCTGAAGACGTAGACCCGGCCAGGGCCAGGTCGCTCT
      < L E N R W S P K L E A V A D H V V P S F V Y G V L A L D S K

44380 TGGGGGTGCTCGGGGCTTCCTCCTCACCCGGATCACCCGCCCCATCTCGGCGACGCCGAAAGGCGTGCGGGGTCGGCGACCCGGGGTC
      < P H E P K E E V G I V R G D A G M E A V G F A H P D A V R T

```
44472 AGCATGATCTGCGGTGCGTGCTCCTGCCGGAGAGCGCTGCGACGATGTCCTTGATCCCGCCGACGATGAAGTTGTGCCGAGGTACATGAG
      <L  M  I  Q  A  H  P  R  E  Q  R  F  R  E  V  I  D  K  I  G  G  V  I  F  N  D  G  L  Y  M  V

44564 GAAGTCGTCGTCGCCGAGGTAGTCGCGGAGATGAGCACGGCGTCGCCAGCCGTGCCAGAGGCCTCCTGCGCAGGTAGGTCACCTGGAGGC
      <F  D  D  D  G  L  Y  D  R  S  I  L  V  A  H  A  L  G  R  P  A  E  Q  P  L  Y  T  V  Q  L  G

44656 CGAACTGGGAACCATCGCCACCGGACCACGGCCTGAATTTCGGGCGCCGGTGCTGCCGACGACGATGCCCACCTCCTCGATACCGCCTCACGAATA
      <F  Q  S  G  D  G  V  V  R  Q  I  E  P  A  T  S  G  V  V  I  G  V  V  E  E  I  G  G  E  R  I

44748 GCCTCGAGCCCGTAGAACACAGCACCGGCTTGTTGCCACGGGAATGAGTTGTTTGGCGGAATGTGGTGATCGGACGCAATCTCGATCCCAC
      <A  E  L  G  Y  F  L  V  P  K  N  A  V  P  I  L  Q  K  A  S  T  H  T  I  P  R  L  R  S  G  V

44840 CCCTCCCGCCAGGACCAGGCCTTCACGAACGACGCCCTCGAAAGGATGGGACGAGACGGGGTCGCTGGTTCACGAGCACTCCAGGGGTCACGG
      <G  G  A  L  V  L  A  K  V

44931 TGGACTGGGCTCTTCGTGAACGTACCGAAGGATCACTCGTGATTTCCCTACTTATGGGCCACCGAGGTGTGATCGGTGGATCTCTATGCGT
                                                                                    <·  A  D

45022 CCGGCCATTTCCGCAAACGGGGGCCTGGCCGGCGGCGGCGTCCTGGAGCTTGAGCACGGGCCGCCGTGTCCGGCGGCTGGCC
      <A  M  E  A  F  P  P  R  A  P  G  G  G  V  L  E  L  V  A  A  L  G  H  V  T  D  P  P  S  A

45114 GGCAGCAGCAGGGTCTGCAGGCCGTACACCGGCGTCGGCCAGGTGTCGCCCACCATCAGCGCCGTCCGGGGCGACCTTCAG
      <P  L  L  L  T  Q  L  G  A  Y  V  A  G  G  D  A  L  T  D  G  V  M  L  A  R  E  P  A  V  K  L

45206 CTCGTCGCAGGCGGTGCGGAAGATCGGGGATGGGCTTGACCGCCCCCACCTCGTGGGAGAAGAGACGTAGGCGTCCGCCATCC
      <E  D  C  A  T  R  F  I  R  P  D  P  K  V  A  G  V  E  H  S  F  V  Y  A  D  V  L  E  A  M  G

45298 CGTACGCCGCGAAGGTGGGCCGCAGGTCCCAGGCGATGTTGCTGACCACGGGCCAGTTCCGCGGCAACTCCGCCAGGACCGGG
      <Y  A  A  F  T  P  R  L  D  W  A  I  N  S  V  V  A  T  G  C  G  R  R  L  E  A  L  V  P

45390 GCGGGCGTCGCGGTAGGGCGTAGGGCAGCCAGCCGTCCGTGCGGAACAGCCGGCTCGGCGAGCGGCCGGATGGGGCAGGTCGACGGGTGGA
      <A  A  D  R  Y  P  L  W  G  D  T  R  F  L  R  D  Y  L  A  E  A  L  G  P  H  P  L  D  V  T  S

45482 GAGCAGGCCCACGTACGCCGTGCGTTCGGGCGTGCGTGCGGAGAGGTCCCGGCGGGGCGAGCCCGGCGGCGGGGACGGCGTGCGGCT
      <L  L  G  V  Y  A  S  R  H  T  E  P  S  L  D  R  R  A  Y  V  E  A  L  G  P  P  V  A  H  P  E
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FIG.11A(40)

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45574 CCGGCCCGCCGGGGACGGCCGGCGCCAGCAGCAACCGGTCAGGGCCTCCTGCTGCGCCGGGTCGAGCTGGAGCGCCAGGTGGCCGCGCC
       <  P  G  G  P  R  G  A  A  L  L  L  G  T  L  A  E  Q  Q  A  P  F  L  Q  V  G  V  T  A  A  A

45666 GCCCGCCAGCGCCAACGCTGCGGCAGTTCCACGGGCAGGGCCAGTTGCCGGAGAAGTGCCGGAACAGCAGGACGGGTCGATCGGACGGGGCAGGGGGTCGT
       <A  R  L  W  R  Q  P  L  E  V  A  F  L  T  G  S  F  D  F  L  V  A  D  I  P  R  P  L  P  T  T

45758 CATCGCTCTCCTCGGTGCAGCCGGCGCTCAGGGCGGCACCAGCCTGGCAGCGACCAGCCGGATGTCCATCATGGAGGAATGCGCCGGGTCG
       <M

45848 GGCGCGCCGCCATGGCCGCGGTCCGGACGACGAGGCATTTCGGTCACTCTTGCCTTCTAGGCGGATTTCTTCAAAGATGGCTGTCAATTC
                                        >  V  T  R  T  A  L  R  R  L  L  A  A  G  L  A  S  L  A  T  A  A

45940 TTCAGGGATCCTGGAGGCATCCGTGACCGTACCGGACGCCCTGCGCCGGGTCTGCGGCCTCGCCAGCCTGCCACCGCTGC
       >  A  T  L  V  A  T  A  G  P  A  A  A  A  T  T  P  G  I  D  V  S  H  Y  Q  G  S  I  N  W  T

46030 CGGCGACCCTCGTCGCCACGGCGCCCGGACCGGCCGCCGCCGCCACCACCCCCGGCATCGACGTGTCCCACTACCAGGGATCGATCAACTGGACGA
       >  A  T  L  V  A  T  A  G  P  A  A  A  A  T  T  P  G  I  D  V  S  H  Y  Q  G  S  I  N  W  T

46122 GCGTCCGCAACGCGGGCATCCAGTTCGCGTTCATCAAGGCCACCGAGGGTACGAGCTACAAGGACCCCAACTTCAACGCCAACTACGTCAAC
       >S  V  R  N  A  G  I  Q  F  A  F  I  K  A  T  E  G  T  S  Y  K  D  P  N  F  N  A  N  Y  V  N

46214 TCCTACAACGCCGGAGTGATCCGGGGGGCGTACCACTTCGCCCGGCCGAACATCTCCTCCGGGCCAACTACCTGGCCAGCAA
       >S  Y  N  A  G  V  I  R  G  A  Y  H  F  A  R  P  N  I  S  S  G  A  T  Q  A  N  Y  L  A  S  N

46306 CGGCGGGGCCTGGTCGGCCGACAGTCGCACCCTGCCGGCGGCGCTGGACGTGGAGGCCAACCCGTACAGCGGCGGCACGTGCTACGGCCTCA
       >  G  G  A  W  S  A  D  S  R  T  L  P  A  A  L  D  V  E  A  N  P  Y  S  G  G  T  C  Y  G  L

46398 GCACGTCCGGGATGCGTAGCTGGATCCAGGACTTCCTGAACACGTACAAGGCCCGCACGGGTCGGTCATCTACACCACCAGCAGC
       >S  T  S  G  M  R  S  W  I  Q  D  F  L  N  T  Y  K  A  R  T  G  R  Y  A  V  I  Y  T  T  S

46490 TGGTGGAACCAGTGCACGGGCTCCTGGACTGGACCCGGTGGGCGTCCGGGATCAGCGGCATCAGCGGCAACGTCGACCGCAACAACTGGAACG
       >W  W  N  Q  C  T  G  S  W  T  G  P  W  A  N  H  P  L  W  L  A  R  W  S  S  T  P  G  T  L  P

46582 GGCCCGGCGGCTTCGGTCTGGAGCTTCTGGCAGTACAACACCTGACCCGGGATCAGCGGCGTCTCGGGTAGCGGGTTGGCGGCAGCGGAACGG
       >  A  G  A  S  V  W  S  F  W  Q  Y  T  A  S  G  S  V  S  G  I  S  G  N  V  D  R  N  N  W  N

46674 GCGACCGCACCCGGCTGATCGCGCTGGCCAACAACACCTGACCCGAACGCCCGGAACGCCGAACAACTGGAACG
       >G  D  R  T  R  L  I  A  L  A  N  N  T  ·
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FIG.11A(41)

46765 ACGGTCGGGCGGCGGTCGGCTGCCGGCCGTCGCGCCCGGCCCGCGCCGGCCATCCGGTCTTGCGGCCCGGGGGGTGGCC

46857 CGGCGTGCCCATCCGGCAGGCGGCCACGCGGCCGGCCACGCGCCGACACAGCGGCGAAGACCCGGCTGACCAG

46949 CAGCAGCACCACGTCGCCGAAGGCGACGAGCATCCACGTGCCAGCCCGGGTCGAGCGTCCTGCTGTCCCATGTCGCACCTCTCG

47041 CATCGTCCGGGATCAGAGATACCCCGTTCGAGCGAACATGCGCAAGTACATGGACATGCGCTGCTCAGCGGGGCCGAGTCGGC

47133 AATGGACGGCCCCGGCCAGCCCGGGGCGTCAGTCGACCCGGTCCGGCTTGAAGCCCTTGAAGCGCTTGGCGATCCGGATCAGGTGCCAGT

< · D V R D P K F G K A I R D F D A L R A Q W D

47224 CCTTGTTGCGCACCTCCCACCGGAGGGCGTACCCCGGTTGCGGCCGTGTGCTGGCGTGGATCGGAAGCCCGGTTGCGGACGTGCGTCCCGG

< K N A V E W R L A Y G R N S A T V F G R N R V H I R T G D R

47316 TTCTCCAACCACTCCCAGTCGCGCACGTCTTGTAGTAGTCGCAGCGCTTGATGCTCAGATACTGGTAGCCGTTGACGTAGTTCTTCCGGGC

<N E L W E D A C T K Y Y D C R K I S L Y Q Y G N V Y N K R A

47408 CGGTTCCTTCTCTTTCCAGTCGGCGTAGGCGTCGCCCTCCGGGGTGCTGGTCCACTGCACCAGCAGCTGCCCACCCGTCGCGCTCGTGTCGA

< P E K E K W D A Y A D G E P T S T W Q V L L E G V G D R E D F

47500 AGACGATCGTTCTGCTGCCCCACGGTCTGCCGCCACCGGCGAGCTGCCCGGGTCCTTGTGCAGGAGCCAACCC

< V I T N Q G V S R R V W G K P L P L S F G A P D K H L L W G

47592 TCGGGCAGGGCGTTCGGGTCCACGGACGGCTGGCAGACGGGCTGGGCTGTGGGCGGCCGACGGCGT

<E P L A N P D V S P S A S P T P S P P A A S S T A P A A S P T

47684 CGGCGTCGACACGCCGCCCTGCGGGGTCGGGGTCCCGGGTGTCGTCGTCGTCCGGGCGGCGCCGGCCACCGGCCAGGCCGA

< P T S V G A Q P D G G P G P D D D G S R G L L P V A A L L G I

47776 TCAGCAGCACCGCGACGAGCGCCGCCGACCGGCGCCGACCAGCCGGCGCCTTCGTGCCGACGACGGTGCCCCCGTCGAC

< L L V A V L A G V L L G R R R E P K T G G V V T A R G T S

47868 GAGAGTGCCGGCGGCCGGAGGGCCGGCGGGCCCGGCAGCACCGAGTCGGCGGCGGCCTCCTCGGCGGCGCACGGGCGGCGGCTCGGGGCGGCGG

<S L A P G S A A P L V S T P A A E E R P A V A P E R A P P

47960 CGAAACGGGCACAGCCGGCGATCGGCCCCGGAGTCGGCGGCCGGTGTCGTCGGCCCCGTCGGCCCCTT

<S V P V A A G P D V R T D D A R T D D A A R G A A P A G D A G E

FIG.11A(42)

48052 CGTCCCCAGCCTCGGCGGCCCGGTCCGGCCGCGGCCCGTCACTCCCTCCGGCCGCCGGTGCCGCGAGCCTCGTCGGCGGTGGTCGGCGGGGTCG
< D G A E A A R D A P P G D S G G A P T G A A E D A S T A A D

48144 GGGGCGGGGATCTTCGGGTGGGATCGGCCGCCTGCGGGCCGAAGTCGGTGACCTTCGGCGTCGGCGCTCGGCAGGTCGAC
<P A P I K A T P D A A Q P G F D T V K A T P D A D A S P L D V

48236 CATCGCGGTGTCGGCGCGGCGGTCCACCCCGCGCGGGACCTTCGCGGTCGGCGTCGCCGCGCCGCGCCACCGGCGGCGGCAA
<M A T P A A D V G A P V K A T A D G G G V G A A A G G A A L

48328 GACCACCTTCCGGGGTACGCGGTGCGGTGCGGGGGCCGCGGCCGGTGCCGTGTTCGGCGGGCTGGGGCACCGGCGGTCGC
< G G E P T R P A P P A A P R G T R Q E A P R P A P V P P R

48420 GGCTCGCGCGGGCCGTTCGGCGCGGCCGGTACGCCCGGCCGGCGTACGCCCGCGTGAGCGGAGATGGTCTTGGCGCGACGCCCGGCGCCGCAGGAGCCG
<P E R P G N P G P R R V G D L L S I T K A R R G A A R R L L R

48512 CTCGGCCACCTGCGCTCGGCGTCGATCGCTCGGCCGGGTCTTGCGGAGCAGCCCGTTCAGCACCGGCCGCTTCAACGGGCCGGGTTCCTCGGCGGCG
< E A V E A D I R E A P D K R L L G N L V P K L P G A N R P P P

48604 GCATCGGCTCGGTGGCCAGCCCGCGCCAGGGTGGCGATCGCCGGCCGTTGCCCTCCACCGCGTAGAGCGTCGCG
< M P E T A L A A L T A I A S P R A F P S K G E V A A Y L T A

48696 CCCAGCGACCAGAGGTCCGGCCTCCGGGGCCTCCGGGGCGATGGTACGCCGGGAGCCCAGCACCATTCCGGT
<G L S W L D A E P G A T G D R A R E P A I Y A P S G L V M G T

48788 CCGGTCACGTTCGGGTCACCGGGGATGGTCGCCAGGCCGAAATCGGTCAGCACCGGCCGTCGGTGCCGAGCAGCACGTTGCCGGCT
<R T V N P D G P I T A L G F D T L V V R G D T G L L V N G P K

48880 TGATGTCCGGTGCATGACGCCGGCCCTTGTGCCGGCCTTCAGCGCGCCGAGCACCCCAGGCGGCGATCTCGACCGCCTTGGCCGGTGCGGCGACACC
< I D R H M V G A K H A A K L A G L V G L G I E V A K A P S V

48972 GGCCCGGTCCTCCGCGGAGAGTGTCTTGAAGGGACTTCGACGCACGGCCACGTACTCCACGGGTCGCGTGCTGCGTGGTGCGCAGAACGTCGAA
<P G D E A L T D Q L S K S A V Y E M V I W P D G D T R L V D F

49064 GATGCGGACCACGTTGACGTGGTTGAGTCGCGCGATGGCACGGCCGTTCCCGCAGCGAGCGTCCTCGCGGCGGTGA
<I R V V N V H N L R A I A R A E R L S R E R M E R E E P T L

FIG.11A(43)

49156 GGCTGGGCGGCGGGGACCAGTTCCTTGATGCCACATCCGGTGCAGCACCTGTCGCGCGCCTTCCATACCGACCATGCCACCCTGACC
         < S P P P V L E K I A V D R H L V E D R A K W V R G M

49247 GAGCGGGCGAAATCAGCGGTACCGGTCGGCAACGAGTTGGGGAAGCGCGTTGACATCGGTGGACACGGTACCCGGCGGCGGCCCGCGCAC
49339 ACCGGCCGGCACGCCACTGTGCGACGAAGGTCAAGTTCGCGACGCGTACGCTGAACGGGCATGTCGCCGGTGTTCCGGGGTGACCC
49431 GGGGCGGTTCCGACCGCGCCGAGGAACTGGCCGCGCTGGCGTCATCGTCGCCGCTCCGCGCCGCGCCTCCGGTCCGCGCGCCGCCG
49523 TCGGCCTGGGCACGCAGCGCGGTCGGCCCCGGCGGTACGGTGCTCGCCGCCCGGGAGCCTGGCGGGGTCGACGCACACCCGTTAACCTCACTCAGGGA
49615 TCGCCAGCATGTGGCCAGTGTGTGGCCCGAGGCGGGTGGCGGGGTCGCAGACCCGTTGAGCGGCTACGGCAGCATCGAGGCCGAC
49707 GACGATGCCGTGACGGATAGGGAGGGGTCGATGATTCCCGAGGAGGACCGACCAGCACCCTGGTTGAGCGGCTACGGCAGCATCGAGGCCGAC
49799 ATCCGCCAGATGCGCGAGTTCGCCGACAAACTCCAGGCGGAGGTCGAGCGGGAAGTGAGCGGGAACTACGCACCGCATCTGTGTACATAGCGACGACATGAA
49891 GGCACAGATCCCCAACCCCGACGCCTTCGCCGACGCGCCACCGGCCACCTGCCAACCTGGCCCGGATCGCCGGCCGGCGCCTTCTCCGCCGCT
49983 TCTGGTCCGTCGGTGGGGCGGTGAGCGTGGAGCGCGGGCCCTGCCAACCCGGCAGGGCGCGGGCAGGGCCGCTCTGCCCGACCAGCCCGGA
50075 CGGCGTCTCCGACGTGGAGCGGCGGGTGGCCCGACGTTCCGGCCTCCACCGACGTCGCCGGGGCTCGGGGCGCTGACCTGCTGAG
50167 CGGCGGGGCCGGGGGTCGGGTGGTGCTGCCATGATCGAGCGGGCACTGGAAGCAGGTTTGCGACCTCGCGGCAGGCCCACC
50259 CATGTGGGCGGTGCATCCAGGACCACGAGACCGCGGGCACTGGAAGCGCGACCCAAGCGCCGCGCCGGCGTACCTCGGCGAACTGGAC
50351 TGGGCGCCTCAAGGAGTACCGGCGCGGCTGGCCGAGGCGTGGCCACCGGCGCGCCGCGCCGGCGACCAGCAGCGCCCG
50443 GACCTGATCGACAAGGTGCAACGCCGCTACACGACGAGTACGTGGAGAAACTCCAGCAGCAGAAGCGGGCGACTACGCCGAAGGCGCTGA
50535 CACCGAACTCAAGCCGCTACAGACCGGATACGCCGATCCGGAACGCGAACAACCGGATGTCTACGAGAGCAC
50627 TGGGCAGCCGGCTGCCGGACAAGCCAATGTCTGCCCCGTATTACCAGTCCCAACCATTAGGCCTTCAATTCCCTCAGCAAGCAGCCACGCCCTG
50719 GAACTCCAACAGGCCCAAGCAATGCTCCGGCCAACCCCCTCCTCCGCACCGATGTCCCATCGGGGAATCGGACAGGCTCAAGCGCTCAGCAAGCTCTACGAGAGCAC
50811 AGGCACGCGCTCCGGTCATCCCGCCGTATTACCAGTCCGTGTACTCGGGGAATCGGACAGCTTCGCCATCGGGTCTCCATTTCTCCGGC
50903 TTCCTGTCCAGAGCGCACCCGCCAAACAGGTCCTGTACTCGGGGAATCGGACAGCCTCCCGGCCATCGCCCCCACTGGACGAGG
50995 ACCGGCCACCCAGTGACATCCAACCCGGCAGGAGGTGCTGGCCCTACCCTCCGCGAACTTGCCACCTGCCATCGCCCCCACTGGACGAGG

                                                                          junction marker

51087 CAGCACAAACCGGCCCAGGTAGGAAACCAGCCCCGCTCAACCAGTCCTCAGCGCCGCTGATCGGCGGCGGGGCCCGCGA
51179 TGGGGATTAATCAACCCCTTGGCAATACTCCTCGCGAAGGATCAACCCAATTGGAGGGGTGATCGGGGGCGGTGGGGGCTGGAACCTCACCA

FIG.11A(44)

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51271  ACGGGGCTGCAGGCACTCGCCGCCCGGGCTCGGGACGTGGTCCCACTTTAACCTGACCCCTGCGGCGCCTCCGAATGGCGCACGCGCAAGGCGT
51363  CGTAAACACCTTAGGTCTGAATGGTGAGCCGCTCACGCTCATCCCCACGCGCGAGCCGGAGGCGGATACTGACGCCGCTACTGGGATCCCGACCATC
51455  CATGGGCAACCAGCAGGGCGGTTCCTCCAGTAGTCCGCCCGCCCGAGGCGGAGGGACCAATCGACCAGGCCAGCTATTGGCTTCGACCGG
51547  TGAAAAACGCTCCTCCAGCGAGCGGGCGCTACCTTCACCTTCCTAGCAACATTGATGGTTGCATCAGCGTACGCCCGAGCGCCGTGCGTGCGA
                                                                                    >V  R  A

51637  GTCCTGAAACCGATGGTGCCTTGCGAATACGGGCACCTTAACTACCTGAAGGCGGCAGAAGCTCAGAAGCTGTCACTGGGA
      >S  P  E  T  D  G  A  L  R  I  R  A  D  Q  W  H  L  N  Y  L  K  A  A  E  A  Q  K  L  S  L  G

51729  GAAGGGGTTGTAGTAGCGGTCCCGGATACTGGCGTTGATCCACACCCGACCTTCAGCGACATCTAATCAAAGGGATTGACATCATTCCCGG
      >E  G  V  V  V  A  V  P  D  T  G  V  D  P  H  P  D  L  Q  R  N  L  I  K  G  I  D  I  I  P  G

51821  GGGCAATGGAGATGGCCAGAAAGATCACGCAACAGTCACGGCCACTAGCATGGCTGGACTAATCGCAGGGCCAGAGGCGGCGCCT
      >G  N  G  D  G  Q  K  D  R  N  S  H  G  T  S  M  A  G  L  I  A  A  H  G  G  Q  S  G  A

51913  TAGGCATAGCACCCAGAGCACCAAGATCATGCCAATCCTGGTCTTCCGGTCGAACAACCTCGGTGATGCGAGACGGCTTGGCTGCGGGGTATAGAA
      >L  G  I  A  P  R  A  K  I  M  P  I  L  S  S  A  S  N  N  L  G  D  A  D  G  L  A  A  G  I  E

52005  TTTGCAATCTCGCATGGGGCGGATGTCAGCCGCCGGGAAACAGTCTCCAGCGGAGGCGGCGCCAGCGTTGACTCATCAAGGCAATCAGAGAGGGGTCGC
      >F  A  I  S  H  G  A  D  V  I  N  V  S  S  G  G  G  A  S  V  R  L  I  K  A  I  R  E  A  V  A

52097  CGGCAGAGACATTGTAGTTGTCGCAGCCGGCGGGGAAACCGCCGGGAAGACAGTCCCGAAGACATGACAATTGGCTATCCAGCCAGTCGTCTCGCAGTTG
      >A  D  I  V  V  A  A  A  G  N  S  P  E  D  M  T  I  G  Y  P  A  S  E  E  G  V  V  A  V

52189  GCGGAATTGATCGACAGGGAGAGCATGCTTCAGTTTCTGTCGTCGGAAGTTGACTTAGTCGCACCGGCAGTCGACATCTACAGCACC
      >G  I  D  R  Q  G  E  H  A  S  V  S  V  V  G  P  E  V  D  L  V  A  P  A  V  D  I  Y  S  T

52281  AGTTACGACGGGAAGTACTCCAAAGGCACCGGTACGTCCAGTGCCACAGCCGATAGTCGCAGCAAAGGGCGCCAGGGCACGACCAGTACGGCTACGGGCG
      >S  Y  D  G  K  Y  S  K  G  T  G  T  S  S  A  T  A  I  V  A  G  A  A  A  L  V  R  S  K  F  P

52373  CGACCTGCCGCCTCGGAGGTCGTCCATCGCCTCACTGCACGCCATCGACAAAGGGCCCCCGGGGGCACGACGTGCTGGGTCGACC
      >D  L  P  A  S  E  V  V  H  R  L  T  A  T  A  I  D  K  G  P  P  G  H  D  D  Q  Y  G  Y  G

52465  TTATCGACCTGGTTGCCGCGCTTACGGCAGAGACGTAACCCCGGTGGGCTTTGAGTCGGCAGCGGCGGACGTGCCGGACGTGCCTGGGTCGACC
      >V  I  D  L  V  A  A  L  T  A  D  V  P  P  D  V  P  G  S  T
```

FIG.11A(45)

52557 ACGACGGGCGGTCGCCGAGCCGGCAGGCGAGGGTGACGATGGGCAACGGCCCGAGGTCTGGCCACGTTGGGAGTGATCGTGGCTGCTGCGGG
>T T A V A E P A G E G D D G A T A R G L A T L G V I V A A A G

52649 CGCTTGGGCGCTGGTCGCTCGACGGGCGTAGGTTGAGCGACGGACCCGGCACCCCGGGATCAGCCGGTGACCAGCCCTGAGCGCCATGTCG ·
>A W A L V A R R R R L S D D P P P R I S R ·

52740 GCGACATTGGGGGTCGGGGTGGGGGTGGGGGTGGCCGATACCGCTATTTGGCCAGACATGAAGTCGATCAACAGGCAGTGTGATCGGCGGGGG
>A W A L V A R R R R L S D D P P P R I S R ·

52832 GTCGGTCGACGGCCAGGCGGCGTCGACGAGGCGGGGGAAGCGGTAGGGTCGGCGAACGTGCCGAACTCGATTTCACTCCGACTCGTGCTCGC
>V P N S I S L R L V L A

52924 GTCGGGCGAGCCCTGCCCGTCGCAAGCTCCTCCACGCCCGGCATCGAACCCGACGTGCTGGTCAGTGGGGTCGACGAGTCCCAGGTGACCA
>S A S P A R R K L L H A A G I E P D V L V S G V D E S Q V T

53016 GCGAGCGAGCCGAGGATCTGTGCCTGGAGCTGGCCCTCGAAGGCCTGGCCGCTGTCGGCCCGTGCGGCCCGAGCGGCGAGCGGCGGACG
>S E R A E D L C L E L A R L K A Q A V V G R L R P S A D E R T

53108 CTGGTGCTCGGCTGCGACTCGGTGCTCGCCTTCGACCGCGAGATTCTCGGCAAGCCGGCCGACGAGGCGGACGCTACCGGCGTTGGGAGCG
>L V L G C D S V L A F D R E I L G K P A D E A D A T R W E R

53200 GATGCGGGGGGCGCAGCGGGGCGTGCTACACACCGGGGCACTGCCTGATCGACGTGATCCACGAGACGCGCGAGGCGGTCGCCTCGACCACCG
>M R G R S G V L H T G H C L I D V I H E T R A E A V A S T T

53292 TGGCGTTTCGCTGACATCAGGCAGGACGACGAGGAGATTGCCGCGTACGTCGGCAGTGGCCGCGGCGTTCACCATCGACGGA
>V R F A D I S D E E I A A Y V A T G E P L A V A G A F T I D G

53384 ATGGGCGGGGCGTTCCTGGAGGGTGTCGACGGGGTGTCGACCGGGCACCGGGTGGTCCTCGGCCTTCTGCTGCGGCTTCTCGGCGAGCT
>M G G A F L E G V D G D P G T V V G L S L P L L R R L L G E L

53476 GGACCTGCGGATCATCGACCTGTGGACGAAGGTCGCGCCCGGGCGGCCCAGGCGGCGTCGAGGCGGTGGGTACGGTCCAGCCATGACGACGAAGT
>D L R I I D L W T K V A P G G G Q A V E A V G T V Q P ·

>M T T K

53567 CCCTGCCGCTGACCCCGGAACTGCATGCGTACGTGGTGGTGGCCCACGGCTCGGATGCGGATCTGATCGAGGAGACCCTC
>S L P L T P E L H A Y V V V A H G S D P D E V M R D L I E E T L

FIG.11A(46)

53659 GCCGCGGCTGCCGCCGGAGGCGGAGGATGCAGGTGGCCCCGGAGCAAGCGGCGGTTCCTGACGTTCCTCACCGGTTGATCGGGGCGGCGGCGGGC
> A L P A E A R M Q V A P E Q A A F L T F L T R L I G A R R A

53751 GGTGGAGGTGGGCACCTTCACCGGCGTCGCGGCGGTACTGGGCGCGGGGCGGTTGACCTGCTTCGACATCTCGG
> V E V G T F T G L S S L A I A R G L A E G G R L T C F D I S

53843 AGGAGTACACGGGCGTCGCGGCGTACTGGGCGCGGGGCGGTGGCCGACATCGACCTGCGCGATCGGGCCGGGGACACGCTG
> E E Y T G V A R R Y W A R A G V A D Q I D L R Y G P A G D T L

53935 CGCGGGTTGCCGTACGAACGGCACCTGGACTTCGCGTTCATCGACGCGGACAAGGTCGGCTACCGGTCTACTGGGCGGAGTTGGTGCCCCG
> R G L P Y E R H L D F A F I D A D K V G Y P V Y W A E L V P R

54027 CATGCTCCCGGGCGGGGTCATCGCGGTGGACAACACGTTGCGCGGGGCCGGGGTGCTGCCCCGACGGCCATCGCCG
> M L P G G V I A V D N T L R G G R V L A P R D A D D R A I A

54119 CGTTCAACGACGAGGTGATGGCCGACGTCCGGGTGGAGCCGGTGCTGCTGCCGATCGCCGACGGGCTGACCCTGGCCCGGTGCGCTGACG
> A F N D E V M A D V R V E P V L L P I A D G L T L A R V R .

54210 GGGCCAGCCGACGACGATCGTGCCAGGTCGCCGCCGGTCGCCGGTCGTGTGTT
>   < . R V S R A F Q R A

54302 AGGAAGGGGCCCTTCCTATACGGAATGGTTAACAAGGGGCCCCTTCACACCTCAACCTCAGCGACGCTGCGGGGGGAACTGGCGGGGGCG

54393 GCCCAGGGCGACGCCGACGCGGCAAGCACCGCGATGATGGTCAGGCCCTGCCGAGGTCGTTGCGTTGGCCCAGACCTTGTCGTTGCCGAGGCCCG
< A W A V G V A A L V A I I T L G Q W V K D N G L D G A F L A R

54485 GGTGCCGTCCACGGCCCCAGGAGAACGGGTTCCACTCGGCGATGCGCTGGAGCCGCGGGGGCGAAGGTGAGCGGCAGCAGGATGCCGGAGA
< T G D V A W S F P N W E A I R Q L W G P A F T L P L L I G S L

54577 GCAGCAGCAGCCGCTGGGCGACGGTGTTCATCGCGTGTTCATCGGGGCGAGCGAGCGCGTCCTTGACCTTGACTCTTGAGCGCGTACGAGCGGCCGAG
< L L V P Q A V T N M V P A L A D E S K V K L A V G Y S V A S

54669 GTCATCAGCGCGATCAGGGCGAGCATCAGGTACGCCAGCAGTCGCCGATGAACAGGTCGCGAACAGGAGCGCGAGCAGGGTGAT
< T M L A I L A L M L Y A L L L D G I F V R L E F L L A L L T I

54761 GATGACGGCCTGGGCGAGCAGCAGCGACACGGTCGCGGCTGACCCGGGTGACCGCGAGCGCGGCGACCGTT
< I V A Q A L L S V V D R L A R G L L L A L R S V P T V R S R E

FIG.11A(47)

54853 CGATGACGCCGGCGGCGCTCGGCGACTCAGGCGACGAGAGGCCGCCGAAGATGGCCAGCAGCACCAGCAGGCCGGGCACGAAG
< I V G A R L E A I L G F G Q F L G G F I A L L V L L G P V F

54945 ATCTTGTACGCCTCGGCCTCGGGTCGGCGCTTCAGCGGCGGGCTTGAGCAGCGGGGGAAGAGGAGCAGTACATCACCGGCTGGAAGACGCC
<I K Y A E A Q T P A N L A P K L L P A F L L L Y N V P Q F V G

55037 GACGAAGACCAGACCGGATTGCGGAGCAGGAGTTGCATCTGGCGCTGGGCGACGAGCCAGGTGTCGCGGGCGAACTTCATGATCGGACT
<V F V W V P N R L L Q M R Q A V L W T D R A F K M

55127 CCGGGGTGGTCAGGACTCGCGCAGCGAGCCGCCGGTCTTGGTAGGAAGAGACGTCGTCGAGGAAGACGCTGGTGGGCGGCGGTCGAGCTGAGCC
< · S E R L S R G T K T L F V D D L S P R H L E I S S L R

55218 TGAGGCCGGACTGGTCGAGCGTCGGCGCGCAGGAGACCTGCGGGATGGCGGTGGCCCCTCGTCGACGGTCAGGCGCGAGGCCGCCGTGACGGTT
< L G S Q D L R R L V Q P I A T A G E D V T L R L G G G D V T

55310 TCCAGCTTGGTGACGTACGGCTCGGTGTCGAGCAGTTGGGCGGCGACCACCTGCGGGAGGGCGGTGGGGGCGTGGGCGGCGGCGCAGCAGCACCTCGCCGGA
<E L K T V Y P E T D L L Q A A Q P T A A A D L G V L L V E G S

55402 GATCTCCCGCTTCAGCCCGGCGTACCCTCGGCCGGGCCCTCGGCCGACGGTCATCCCGGCGCGCGGATCTGCTCGGGGTCGAGG
<I E R K L G G P T G E A V V E G H D M I A I R D C L A D A E D

55494 CCAGGTAGTGCGTGGTGATGAAGACGGTCATCCCCTCGGCGCGCAGCCGAGCCGGTGTGGGCGGCGACTCTGCGGGTGGGAGG
< L Y H T T I F V T M G E A R L R R I E D W M H A R S Q P D L

55586 CCGCTGGTCGGCTCGTCGTCCAGGAAGACAATGCGGGGGTCGTGGTGCCGCGGCCGGATCTCGACGCGCTGGCCGCCGGAGTAGGT
<G S T P E D L F V I R P D H I I G L A I E V R R R Q G G S Y T

55678 CTTGCACTTACGGTCGCGGCTACTCGGTGAGCTGGAAGGCGGCCAGTGGAAGGCGGCGTCGGGCCTTGCCGATGCCGATGCCGTACA
<K C K R D A Y E T L Q F A A L A R E A R R L A D A K G I G Y M

55770 TCCGGGCGGTGCCAGGACCAGTTCCTCGCGGAGGTCGGTGGAGTCGGCCGGTGCCCCTGGGCGTGCTGCCCGACGCCGGACGCACCTCG
< R A H L V L E E R A T S D D W T S G G Q A V Y G I R R R V E

55862 GCCGGGGTTCCCGCAGCAGGTCCCCGGCGATGGTGTGGCCGCTGGCCAGCATCCGGCAGGGTGATGAGGGTGATGGGTGGTGTCTT
<A P N R L L D A G A I T A Q G G D P T I L T A L M R L T T T K

FIG.11A(48)

55954 CCCGGGGCCGGTTGGGGGCCGAGGAACCCGAAGATCTCCCCCTCGGCGACGTCCAGGTCGACGCCGGCACGGCGGTCGACGTCTTGTGTGCTGTC
    <G A G N P G L F G F I E G E A V D L D V G R V A D V T K H Q R

56046 GACCGGCGCGGGAGGCGAAACGACTTCCGCAGCCCCTCTGGTCTTGGATCATCTTCGCTCCTTGGTCGTGTCCTTAGCGGAGACCGGGGCCGGCCCTC
    <G A R S R F S K R L G R T Q I M

56136 TCTCCGGGACGCGCCACGCGGTGGCCCGAACGTCGCGCCGAGGCTAACGGATATAAACTCTAGTCAACTTTGATTAATGGCGA
    <• R S I V E R T L K S • H R

56227 CCGTCGGCCCCCTCCCCCAGTTCCAGCGTCCTGACTGGCCAACCCTTGGGCAGATACGGCACGGCCTGATCCGGTCGGCGACCCG
    <G D A G E G V N W G D Q S A L G E P L Y P V G A E I R D A V R

56319 CTCACACCAGGCCACCTCGACTCTCCCGGGCAATCCACCAGCTCGTACATCCAGCTTGGAGTGCCGGGATCCAGGAGG
    <E C W A V E V E G R A I W L E Y M W S V G V P K S D R I W S S

56411 ACTCCATCGAGGCACGCATGGTTTCGACACTGGTTCGGCCCCGCCCGCGACTGCCCAGCGCGCCCACGCGCTCGGGCCTGGGCAGCGCC
    <E M S A R M T E V S A R L V Q G R S R L A A V A E P R P L A

56503 GGCAGGAACGCGAACGCGCCACGAACGGATCGTCGTCTGATGATTGCCCCACCACAGGCCGCGCAGCAGCGTCTCGAACTCGTCGACCCC
    <P L F A F A A V F P D S T Q H N G W W L G R L L T E F E D V G

56595 CTTCGGGGTGATCTCGTACGTGTCCGGCCCCGCCGCCCTGTCGGTGGCCGACCTCCGCGGGAGCAGCCCCTCCTCGCCGAGCTTGC
    <K P T I E Y T T R A R A G V Q E T A V E R L L G E E G L K R

56687 GCAGCGCGTGGTAGATCGGCCGGCTGCACGTTGGCCCACTTGTCGGCACCCCAACTGAGCAGCTCGGCGGACGTCGTAGCGTGCACC
    <L A H Y I S G P Q V N A W K D A G W S L L E R R V D Y G H V

56779 GGCTGCATCCCACTTGACACCGCCAGGCCGAGAATCATCATGCGAGTGGCAGACACCGGAAAAGAGTATTAGACAAGTTTGACTATCCAAGCATCTG
    <P Q M W K V L G L I M M

56870 GGCAGTGCCTCATCCCACACTGAGGCGATCGTTAGGGCCACGACGCGGCCGATAAACTCCCGTCAGTAACATCCCGGGAGGAGCCACGAG

56961 GTGCGCAAGGTACTCATCGCCAACGAGGCGAGATCCACGAGGCGTCGCGCCTGGGCAGCGTCGCCGTCT
    >V R K V L I A N R G E I A V R V I R A C R D A G L G S V A V

57052 ACGCGGACTCCGACCGGGACGCGCCCTGCCCATGCACGCCCTGGCCGACGAGGCGTACGCGCTGGGCGGCGACACCGCCGAGACGTACCTGCGG
    >Y A D S D R D A L H A T L A D E A Y A L G G D T A A E T Y L R

FIG.11A(49)

57144 ATCGACAAGCTGATCGCCGTCGCGGGCACAGGCCGGGCCGACGCCGTCCACCCCGGGTACGGCTTCCTCGCCGAGAACGCCGACTTCGCCCA
>I D K L I A V A A Q A G A D A V H P C Y G F L A E N A D F A Q

57236 GGCCGTCCTCGACGCCGGGCTTACCTGGATCGGCCCGACCCCACAGGCCGATCGCCGACCTGGGCGACAAGGTCACCGCCCGCCACATCGCCC
>A V L D A G L T W I G P T P Q A I R D L G D K V T A R H I A

57328 AGCGGGGCGGGCGCGCCCTGGTTCCCGGTACCTCGGACCCGGTCGGCAGCCCGGACGAGGTGATCGCATTCGCGGTCGACCACGGCCTGCCG
>Q R A G A P L V P G T S D P V G S P D E V I A F A V D H G L P

57420 GTCGCCATCAAGGCCGCCTTCGGCGGCGGCGGCCTCAAGGTGGCCCGCACGATGGAGGAGATCCCGCACCTGTTCGAGTCGGCCAC
>V A I K A A F G G G G R G L K V A R T M E E I P H L F E S A T

57512 CCCGGGAGGCGGTCGCGGCCGTTCGGCGGCGAGTGTTCGTCGAGGCCCAGGTCCTGGCCG
>R E A V A A F G R G E C F V E R Y L D Q P R H V E A Q V L A

57604 ACCAGCACGGCAACGGCGTGATCGTCGTCGGCACCCGCGACTGCTCGCTGCAACGCCGCCACCAGAAACTCGTCGAGGAGGCCCCGCCGTTC
>D Q H G N V I V V G T R D C S L Q R R H Q K L V E E A P P F

57696 CTCACCGACGCCCAGCGCCGCCAGATCCACGACAGCGCCAAGGCAATCTGCCGGGAGGCCGGGTACCACGGCGCCGGTGGAGTACCT
>L T D A Q R R Q I H D S A K A I C R E A G Y H G A G T V E Y L

57788 GGTGGGCACGGACGGCACGATCTCCTTCCTTGAGGTCAACACCCGCCTGCAGGTCGAGCACCCGGTCACCGAGGAAACGCCGGCATCGACC
>V G T D G T I S F L E V N T R L Q V E H P V T E E T A G I D

57880 TCGTCCGCGAGCAGTTCCGGATCGCCGACGGCGAGAAGCTGCGGCTGCCGAGGATCCAGCCCGCGCGGGCACTCCATCGAGTTCCGGATC
>L V R E Q F R I A D G E K L R L A E D P T P R G H S I E F R I

57972 AACGGCGAGGATCCGGGCCGCAACTTCCTGCCGCCCGGGGTGTGCTGGGACAC
>N G E D P G R N F L P A P G T V T A L R L P T G P G V R V D T

58064 CGGCATCTCCGCCGGCGACGTGATCGGCGGCAACTTCGACTCCCTGCTGGCCAAGGTGATCATCACGGGCGAGACCCGCACCGAGGCCCTGG
>G I S A G D V I G G N F D S L L A K V I I T G E T R T E A L

58156 AGCGGCCGCGCGGCGGGCGCTGGACGAGATGGTCGTCGAGGGAATGGCCACGGCGCTGCCGTTCCACCGCCTGGTGGTACGCGACCCCGCGTTC
>E R R R A L D E M V V E G M A T A L P F H R L V V R D P A F

FIG.11A(50)

58248 ACCGGCGGCGCCGTTCACCGTGCACACCGGTGGATCGAGACGGAGTTCGACAACACCGTCCTGCCGTTCACCGCGGCCGCGGCCGGCCCCGCCGA
>T A A P F T V H T R W I E T E F D N T V L P F T A A A G P A E

58340 GGGCCCGGCCGAGCGGGAGACCGTCGTGGTCGAGGTGGGCGGCAAGCGGCTGGAGGTGACCCTCCCGGCCGGGCTCGGCGGCGGGTACGGCCG
>G P A E R E T V V V E V G G K R L E V T L P A G L G A G T A

58432 CCCGGGCCCGCGCGGAAGCCGGCCCGGCGGGGCGGGGCCAAGGCCGGGGCCAAGGCCGGAGCCGTCGGGGGCGACGCCCTCACCTCTCCGATGCAG
>A G P A A R K P A R R G G G A K A G A A V G G D A L T S P M Q

58524 GGCACGGATCGTGAAGATCGCCGTCGCGGACGGGGACACCGTCGCCAAGGGCGACCTGGTCGTGGTGCTGGAGGGCGATGAAGATGGAGCAGCC
>G T I V K I A V A D G D T V A K G D L V V V L E A M K M E Q P

58616 GCTGCACGCGCACAAGGGCGGGACACGGTCGGCGGCCTGTCCGCCGAGGTCGGCGCCGTCCTGGCCGCCGGGGCGCCCATCTGCACCATCACCT
>L H A H K A G T V G G L S A E V G A V L A A G A P I C T I T

58708 GAGGTGCAAGGAGGGGCCCCTGTTAACGCATTCGGTATAGGAGAAGGGCCCCTTCCTAACCACGCGCCCGCGCGGGGCCGCCCCAGCCCGGG
>.

58800 TACGCGTACCGGCCCGGGGGTGTTTTCCGGCGACCACCGCGGGGTGAGGACCGCGAGGTGGATGATGGCCAGGTGCGGTTCCTACATGGC
>   > V R F L H G

58891 GCGGGTTCCCGGCCACCGACCTGACCTACAACGACGTCTTCATGGCGCCGAACCGCTCCGAGGTCGGCTCCCGGTTGGACGTGCGACCTGGCCAC
>A V P A H D L T Y N D V F M A P N R S E V G S R L D V C L A T

58983 CTCCGACGGCACGGGCACCACCATCCCGCTGGTGGTCGCCAACATGACGGCGGTGGCCGGCGGATGGCCGGAGACTGTCGCCGGCGGG
>S D G T G T T I P L V V A N M T A V A G R R M A E T V A R R

59075 GCGCACTCGGGTGATCCGCAGGACATCCCGATCGAGGTGGTCGCCAACGTGGTGGCCAACGGCACGGCCACCTGGTCACGACGACACG
>G A L A V I P Q D I P I E V V A N V V A W V K Q R H L V H D T

59167 GCGATCACGCTCGGCCCCACCGACACCGTCGGCGATGCCATCCATCTGCCGAAACGGTCGCATGGCGCGGTGGTGGTGGAGGC
>A I T L G P T D T V G D A I H L L P K R S H G A V V V V D E A

59259 CGGTCGGCCGCTGGGCGTGGTGACGGAGGCGGACACCGTCGGGGTGGACCGCTTCGCCCAGCTGCGCCACGTGATGTCGACGAGTTGCACA
>G R P L G V V T E A D T V G V D R F A W L R H V M S T E L H

FIG.11A(51)

59351 CGGTGCCGGCGGGACGCGGACCGGCGGTACCGGCTCTCGGCGGGCCGGCGGCGGCTCCGGCGGTGGTGGACGGCGGCGACGGCCGG
>T V P A D A D P R T G F D R L S A G R R R L A P V V D G D G R

59443 CTCGTCGGGGTGTTGACCCGCAAGGGCGCGCTCACCGGCGGCGGCGCTGGAGACCCGGTGGACGACGATCGCGGCGGC
>L V G V L T R K G A L R A T L Y T P A V D D R G R L R I A A A

59535 CGTCGGCATCAACGGCGACGTCACCGGCAAGGCCGCGCGGCAAGGCCGCCCTGCTGGAGGCCGGGGTCGACGCGCTGGTGGACACGGCGCACGGCCACC
>V G I N G D V T G K A A L L E A G V D A L V V D T A H G H

59627 AGGCGCGGATGGTCGCCGCGCTGCGGGCCGTGCGCAAGCTTCACCCGGGCGTTCCGGTCGCGGCCGGCAACGTGGTCACGGCCGATGGGGTA
>Q A R M V A A L R A V R K L H P G V P V A A G N V V T A D G V

59719 CGGGACCTGGTCGAGGCCGGCGCCGACATCGTGAAGGTGGGCGTCGGGCCGGGCGGCGATGTGCACCACCCGATGATGACCGGGGTGGGGCG
>R D L V E A G A D I V K V G V G P G A M C T T R M M T G V G R

59811 TCCGCAGTTCTCCGCGGTGCTGGACTGCGCCGCGGCGGCGGCCGTGAACGTGCTGGTTCGCGGCCGCACGTACGAGTCCCGGGTGACCTGTACACG
>P Q F S A V L D C A A A A R D L G R H V W A D G G V R H P R

59903 ACGTGGCGCTGGCCCTCGCCGGCGGGTCGAACGTGATGATCGGTTCGTGGTTCGCGGCCACGTACGAGTCCCGGGTGACCTGTACACG
>D V A L A L A A G A S N V M I G S W F A G T Y E S P G D L Y T

59995 GACGCGGGACGGCCGGAGGTACAAGGAGAGCTTCGGGATGGCCTCGTCGCGGGCGGTCAGCGCGGTACGGCGTACGGCAGCGGTTCGACCG
>D A D G R R Y K E S F G M A S S R A V S A R T A E D S A F D R

60087 GGCCCGCAAGGGGATCTTCGAGGAGGGCATCTCCTCGGCCCGGATGTACCTGGACCCGCGTCGAGGACCTGATCGACGAGA
>A R K G I F E E G I S S A R M Y L D P D R P G V E D L I D E

60179 TCATCTCCGGGGTACGCAGCGCGTGCACGTACGCGGGCCGGTCGCTGGCGGAGTTCGCGGAGCGCGCTGGTGGGGGTGCAGAGCACG
>I I S G V R S A C T Y A G A R S L A E F A E R A L V G V Q S T

60271 GCCGGCTACACCGAGGGGATGCCCCTACCGACGAGTTGGTGACCCGCCCGGCCCGGGGGTGAGAAGGGTTCCCTCTCTACGGGAGGGGTCAA
>A G Y T E G M P L P T S W .

60362 CAAGGGGCCCTTCGTGCGCGGGTATCGGGTGTCGACGACTGCCGCGCACTGAGCGCGCCGCCGCCGTGAGGGCCC

FIG.11A(52)

60454 ACCGAACGGGGCGCGGGGTCAGTCGAAGAGGCGACGGATGACGGTCCGGGGCCGGGGCCGGTGCCGGGCCGGGAGCGCC
       < • D F L R R I V T R A A A E P D P G T G P P L A

60545 CCGGCCAGCCAGAGTGTCACGAAGCCGTGTGCACGATCGACCAGGGCGGCCAGGGCCGGTCCGGATCCTCGGTTCCGGCGGCGGGGAG
       <G A L W L T V F G H V I S W A A L A D A E Q D P T E R R P L

60637 GGCGGCCACCCGCAGCGCGCCGATCACGGGGCGGCGGCTGTCACCTGCGCGACGGTAGAGCTCCGGGGCGGAACA
       <A A V G A R L A A G A R D R A A T V E P D D R R Y L E P R F M

60729 TCACCTGCGAAGTGGGCCCGGGTGTGGTCGACGCGGAACCGGACGTACGCCGGGTCGAGCGGTCGCCGCCACAGCGCCCCGGCC
       < V E F H A R H D V A F R V Y A V G A D L L L D G A E C L A G A

60821 AGCAGGTCGAATCCCTCGACGGCGAGCGGGTGAGCACGCGCCTTGTCGCCGAAGTGGTGCGCGGGGGCGGGGTGCGAGACCCCGGCCCG
       <L D F G E V A L A T L L G A K D G F H H A P A A H S V G A R

60913 GCGGGCCAGGTCGCGCGCAGGCTCAGGGCGGCGGCCCGGGCCGTCGGTGATCGCGGCCTAACTTGTCATTGACAAGTCACCGT
       <R A L D R L S L A A P G A D T I A D V A A L L A R R L D G H

61005 GATGGTAGCCACGGCGGTCCGGTCATGCCGGCAGCCTAACTTGTCATTGACAAGTCAATGCTAGGCAATGACAAGTTG
       < H Y G R P G T M

61095 CCTTCGACCGAGGAGAACCCGATGGCGCCCCTGATCGCTCTCATCGCGGTCGGCCCTGGCCCGACTCGCGGGCTACTCAACGTCGACG
       >M V P P R L P H P G L L V V T G L L E L A G A V A L L

61187 CCCTGCGCGCTGGCCGCCCCGCTGGGTCGGGCTCGCGCCATGTTCGCGCTCACCTTCACCTCCCGACGGCCCGAC
       > V P G T A R W A A A G L G L L L A M F P A N A S A A R R G

61279 CTGGTCGCCATGGTGCGCCCCACTGCCCCCACCGGGGCTGCTGGTGACCGTCACCGGGCTGCTGGAGTTGGCCGGCGGGTCGCGCTGCT
       >M V P P R L P H P G L L V V T G L L E L A G A V A L L

61371 CGTCCCCGGCACGGCCGGGTGGGCAGCCGGCGGTGGGCTGGGGCTGCTGCTCGCCGATGTTCCCGGCCAACGCCTCGGCCGCGCGGGGC
       > V P G T A R W A A A G L G L L L A M F P A N A S A A R R G

61463 TGACCCTGGCCGGCCGGCCGGTGACCCCGCTCGTCCCCCGCGCGCTCCTCCAGGTGATCTTCCTCACGGCGGCGGCGATTTCGTTTGGG
       >L T L A G R P V T P L V P R A L L Q V I F L T A A A A I S F G

61555 CCCTGACTATCAGGGAGCTAACATGACCCGCATGAGCTGATAGGGCTGCGAGACGTGCCACTCGGCCGGCCTGCTGGTGACCGCCGGCCA
       > P •

61645 CGTCGTCGGCCAACGGTGGAACCGCTACCTCGCCGAGGAGCACGGCCTCACCCAGGCGGGCATGGTCACCCTGATGACCCTGGCCCGGCACG
      > V V G Q R W N R Y L A E E H G L T Q A G M V T L M T L A R H

61737 GCGAGCTGCCGCACCGGGCGGTCGCCGAGGCGGTGCTTCATCCGCCGCCACCCTAACCGGCATCGTGACACTGGAGCGCGACGGCCTC
      >G E L P H R A V A E A C F I R P A T L T G I V D T L E R D G L

61829 GTCGAGGCGGCAACGCGACGAGACGTCGACCGGCGCAGCGTGCGGCTCGTCCTGACCCCGGCGGGAACGGGTCGCCGGTCGCCAACGT
      > V E R Q D D V D R R S V R L V L T P A G R E R V A A L T N V

61921 CATGCAGTCCGGACGACCGATGACCTCGGTCGACGCGCCGACCCGGCGAAGGCCGGCAGTTCCTGCTCGAGGTCATCGGCAGTG
      > M Q S G R P M T S V D A D P A K A A V I R Q F L L E V I G S

62013 GAGAGGAACCTCGGGGTGACGGGCCCTGACGGCCGGAGGCTCGGAGCCCGGAGGCCGAGCACGATGGCCTCGCTCTACCTGCCCCACCTGCCGTC
      >G E E P R V T A L D A R P E A P A C .

62105 GACCGCTGGCGGCGGCGGTGATGGCCGTTGCAGTTCGTCGGCACGATGGCCTCGCTCTACCTGCCGCACGATCATCGACCAGGG
      > M A L Q F V G T M A S L Y L P S L N A D I I D Q G

62196 TGTGGCCCGGGGGGCGGACACCGGCTACATCATGCGGACGGGCGGCTGGATGCTGCTGGTCAGCCTGGTGCAGATCGCCTGCTCCACCGCCGCGG
      > V A R G D T G Y I M R T G G W M L L V S L V Q I A C S T A A

62288 TCTTCCTCGGCGCGCGTCCGGCGATGGGCTTCGGCCGGGACGTTCGGCCGAGGTCTTCGCCCACGTCAACCGGTTCTCGCCGCGGAGGTG
      >V F L G A R S A M G F G R D V R A E V F A H V N R F S A R E V

62380 ACCCGCTTCGGGCGCACCCTGCTGATCACCCGCAACACCAACGACGTGCAACAGGTGCAGATGCTCGTCTGTGGTGCCATGCTGGT
      > T R F G A P S L I T R N T N D V Q Q V Q M L V L M S C T M L V

62472 CGCCGCGCCGATCATGAGCGTCGGCGGGGTGTTCATGGCACTGCGGGAGGACGTCGGCCTGTGTCCTGATGAGACGGCCGGCGC
      > A A P I M S V G G V F M A L R E D V G L S W L M L V S V P A

62564 TGGGCGGATCGCCCTGATGCTGATCATCCGGCGGATGGTGCCGGGTTCCGGCTTCCGGCTGATGCAGACCCGGATCGACGCGGTGCTGCGC
      >L A I A L M L I I R R M V P G F R L M Q T R I D A V N R V L R

62656 GAGGCAGATCACCGGCATCCGGGTGGTCCGCGAGCCGTACGAGACGGCGCGCTTCGGCCGCGGAACGCCGCGGTGCTGCACCGC
      > E Q I T G I R V V R A F V R E P Y E T A R F G R A N A D L T A

FIG.11A(54)

62748 GACCGCCCTGCGCACCGGTCGGTTGATGGCCCTGATCTTCCCCGTGGTGACGCTGGTGCTCAACGTCTCCAGCGTTGCTGTGTTGGTTCG
> T A L R T G R L M A L I F P V V T L V L N V S S V A V L W F

62840 GCGCGGACCGGCGGTCGACGCGGCCAGATCCAGGTCGGGCGCGCTCACCGCCTTCCTGCAGTACCTCATGCAGATCCTGATGGCCGTCATGTTG
>G A D R V D A G Q I Q V G A L T A F L Q Y L M Q I L M A V M L

62932 GCCACCTTCATCCTGATGATGGTCCCGCGCGCGGTCTGCGCCGAGCGGATCGTCGAGGTGCTCGACACCGACTCGACGGTGATCCCGCC
> A T F I L M M V P R A A V C A E R I V E V L D T D S T V I P P

63024 GGCCGCGCCGACGGCCGAGGTGACCGGGCGCGGGGAACTGGAACTGCGCGGCGTCCGGTTCCAGTACCCGGGGGCGAGCGCGCCGGTGCTGC
> A A P T A E V T G R G E L E L R G V R F Q Y P G A S A P V L

63116 ACGACATCTCGTTCCGGGCCACGCCCGGGCGCACCACCGCCATCATCGGCAGCACCGGAGGCAAGACCCTGCTGACGCTGATCCCC
>H D I S F R A T P G R T T A I I G S T G A G K T L L T L I P

63208 CGGCTGATCGACGCCACCGGCGCGGTGGTCGTGCTGGGTGGTGACGTGGTGGACGTGGTCCGGGATCTGGCGCCGGATGCGGCT
> R L I D A T A G A V L V D G V D V R D L A P D D L W R R I G L

63300 GGTGCCGCAGCCCGTACCTGTTCAGCGGCACCGGGTACCTGTTCAGCGGGCACGATCGCCAGCAACCTGCGCTACGGCAACCCGGGAGCTGTGGGCCG
> V P Q R P Y L F S G T I A S N L R Y G N P D A T D A E L W A

63392 CCCTGGAGATCGCCCAGGCGCGGGACTTCGTCGCGGAGTTGCCCGAAGGGCTGAACGCCCGATCACCAGGGCGCACCAATATCTCCGGC
>A L E I A Q A R D F V A E L P E G L N A P I T Q G G T N I S G

63484 GGGCAGCGCCAGCGCCTCGCGATCGCCCGGGCCCTGGTCCGCAAGCCGGAGATCTACCTGTTCGACGACTCGTTCTCGGCGCTCGACCTGGG
> G Q R L A I A R A L V R K P E I Y L F D D S F S A L D L G

63576 CACCGACGCCCGGCTGCGCGCGGCGCTACGACGGGTCACCGCAGACGCTGTGATCGTGCTGGTCGCCCAGCGTCTCCAGCGATCGTCGACG
> T D A R L R A A L R P V T A D A T V L I V A Q R V S T I V D

63668 CCGACCAGATCATCGTGCTTGAGGACGGCGGCATCGTCGGGATGGGGCGCCACGCCGAACTACTGGAAGACTGCCCGACGTACGCGGAGATC
>A D Q I I V L E D G G I V G M G R H A E L L E D C P T Y A E I

63760 GTCGCCTCCCAGCAGACGCAGAGCGGGGTGCCGGCATGACGGGCTACCAGCAGCCGTACCGGGATCAGCGGGCCCCACCGCGCGGGCGAGGGGCCGACGCCGAA
> V A S Q Q T A G V P A .

FIG.11A(55)

63851 GCGGCTGCCCTCCGGCAACCAGGGCAGCGGCCCGAGGTGGATGAGCGCCGGAGAAGTCGATGAACTTCGGGCCGTCCAC

63941 CCGCCGGCTGCTGCGCCGGCTGCGACCGCCTCCAGCTGGCCGCGCCATCGTTCTGCTTCTGCTGGTTGCAACGTGTACG
>M S A G M P A E K S M N F G P S T
> R R L L R R P H R L Q L A A I V L L S L V S V G C N V Y

64033 GGCCGAAGGTGCTCGGCCACGCCACCGACCTGATCTTCAGCGGGGTGATCGGCCGGCAGTTGCCGGCAGGCACCACCGC
>G P K V L G H A T D L I F S G V I G R Q L P A G T T A E Q A V

64125 GCGGGCGGCCCCGCGGCGCGGTAACGACAGCTTCGCCGACATGCTGGCCCGGGTGGTGCCCGGGTGGGCATCGACTTCACCGCCCT
>A A R A A G N D S F A D M L A R M D V V P G V G I D F T A L

64217 GGGCCGGGTGCTGCTGTTCGTGCTGGCCCTCTACCTGGCCGACGTGCTGTTGTGGCAGGGCTGGCTGCTCAACGGGGTGGTGCAGC
> G R V L L F V L A L Y L A A S V L L W Q G W L L N G V V Q

64309 GCACGGTGCTGCGGCTGCGCGCCGACGTGGAGGACAAGCTGAACCGGCTGCGCCTACTTCGACCTGCAGTACTTCGACCGGCCGCGGGAGTTGCTC
>R T V L R L R A D V E D K L N R L Q L Q Y F D R Q P R G E L L

64401 AGCCGGGTCACCAACGACAATCTCGACAGAGCCTCCAGCAGACGCTGAGCCAGCTGCTCACCTGCTGCTCACCTGCTGGTCGGCGT
>S R V T N D I D N I S Q S L Q Q T L S Q L L T S L L T V V G V

64493 ACTGGCCATGATGTTCTGGATCTCGCCGCTGTTGGCCGTGTCCCTGGTGTCCCTGGTCGCCGATGTGCGGTGGTCACCAGCCTGGTCGGCGGCGA
> L A M M F W I S P L L A L V S L V A V P M S V V V T S L V A

64585 AGCGGGTCACAGCAGCAGCGGTTCATCGCCCAGTGGACGACGCATACCGGAGAGCTGAACGGCCAGATCGAGGAGGCGTTCACCGGACACGAGCTGGTC
>K R S Q Q R F I A Q W T H T G E L N G Q I E E A F T G H E L V

64677 AAGGTCTTCGGCCGCCAGCGCGAGGTGGAGGCCGCCTTCACCGCCAAGAACGAGGAGCTGTTCCGGGCCCAGTTCATCTC
>K V F G R Q R E V E A A F T A K N E E L F R A S F G A Q F I S

64769 CGGGATCATCATGCCGGCGATGATGTTCATCGGGAACCTCAGCTACGTCGCGATCGCGGTCGTGGGGGTGGCGGGTCGAGGAGTGGGGGTCGGA
> G I I M P A M M F I G N L S Y V A I A V V G G L R V A S G S

64861 TGAGCATCGGCGACGTGCAGGCATTCATCCAGTACTCCCTCCAGTTCACCCAGCCGCTGACCCGGGTCGCCTCGATGGCCAACCTGCTCCAG
>M S I G D V Q A F I Q Y S L Q F T Q P L T R V A S M A N L L Q

FIG.11A(56)

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64953 TCCGGGGTGGCCTCCGCGGAGCGGGTGTTCGCGGTGCTCGACGCCGAGGAGCAGAGCCCGGACCCGGCGGTGCCGGCCCGGGTCGCCGACCA
      > S  G  V  A  S  A  E  R  V  F  A  V  L  D  A  E  E  Q  S  P  D  P  A  V  P  A  R  V  A  D  Q

65045 GCGCGGGTCGCGGTCGAATTCGACCACGTCTCATTCCGGTACGAGCCGGACAAGCCGCTGATCACCGACCTGTCGCTGGTCGCCGAGCCGGGGC
      >  R  G  R  V  E  F  D  H  V  S  F  R  Y  E  P  D  K  P  L  I  T  D  L  S  L  V  A  E  P  G

65137 ACACGGTTGCCATCGTCGGGCCGACCGGCGCCGGCAAGACCACCCTGGTCAACCTGGTGATGCGCTTCTACGAGCTGGACGCCGGCCGGATC
      >H  T  V  A  I  V  G  P  T  G  A  G  K  T  T  L  V  N  L  V  M  R  F  Y  E  L  D  A  G  R  I

65229 ACCCTCGACGGGGTCGACATCACCACGCTGAGCCGCGACGACCTGCGCGGCCGGATCGGCATGGTCCTGCAGGACACCGAGCTCTTCGGTGG
      >  T  L  D  G  V  D  I  T  T  L  S  R  D  D  L  R  G  R  I  G  M  V  L  Q  D  T  E  L  F  G  G

65321 CACGGATCCGCGACAACATCGCTACGGCCGGCCGGACCGGCGAGGAGGAGATCGTCGCCGGGGCGACGTTCGTGGACCGGTTCG
      >  T  I  R  D  N  I  A  Y  G  R  P  D  A  S  E  E  I  V  A  A  R  A  T  F  V  D  R  F

65413 TGCGTAGCCTCCCCGAGGGTCATCGACTCCGGTCATCGACTCCGAGGGCAGCAACGTCAGCGCCGGGAGAAGCAGCTCATCACCATCGCCCGG
      >V  R  S  L  P  D  G  T  D  T  V  I  D  S  E  G  S  N  V  S  A  G  E  K  Q  L  I  T  I  A  R

65505 GCGTTCCTGGCCGAGCCGTCGCTGCTGATCCTCGACGAGGCGACCAGTTCGGTGGACACCCGACGGGAGGTGCTGCTCCAACGGGCCATGGC
      >A  F  L  A  E  P  S  L  L  I  L  D  E  A  T  S  S  V  D  T  R  T  E  V  L  L  Q  R  A  M  A

65597 GGGCGCTGCGCTCGGACCGGACCAGCTTCGTCATCGCCCACCGTTTGTCCACCATCCGCGACGCGGACCTGATCCTGATGGAGCACGGGTC
      >  A  L  R  S  D  R  T  S  F  V  I  A  H  R  L  S  T  I  R  D  A  D  L  I  L  M  E  H  G

65689 GCATCGTCGAGCAGGGCACCCACGAGCAGCTCCTGGCCGCGGCCAGGGCGTACCACCGGCTTTACCAGGCCCAGTTCACCCAGCCGGACCCG
      >R  I  V  E  Q  G  T  H  E  Q  L  L  A  A  R  G  A  Y  H  R  L  Y  A  Q  A  F  T  Q  P  D  P

65781 GCCGCCGTCGGGGACCCCGAGCCCCAGCCCGCCTCGGTCCGCGGCTGACCGCGTCCGGGGCTGACCGTCGTGGCCGTACATCCCGCCAGCTCCCCGACCCGCAG
      >  A  A  V  G  D  P  E  P  Q  P  A  S  V  R  G  .

65872 GGGCAGCTCCCCGGGGCCCCCGGGGCGCGGAAGACCAGAGCGTGGTGCGGGGCAGGAGCGCCGGGCGAGCACGAACTCGTCGTCGGGGCCCAGCCG
65964 CATCGGGGGAACATGTCGTCGGCGGAAGTGGCCGAGGTCGGGGCCTCGATGACGGTCAGTGCGGGCGCGGGGTTCCCGACGTCG
66056 TGGTCCGGTACCGCGCTGCGCATGGGGGAGACGGTAGGGGGAGACGGCCGCATCCGAATTCGGGGCGCCAGCAGCGCCCAGCCGAGACG
66148 CATCCGGTTACCGCGAAGGGGCGACAGGCCGCCAGTCGGCAACCCGGCCGCCTCGGGGCGGCGGCGGCGCCGGCAC
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FIG.11A(57)

66240 GGGACCTGCCGGGGCGGCCCATGGCGGCCCGGTCGTCGGCTACGGGGGGTCCGGTCGTCGGC

66332 GATCCGGTCGACGGCCGCTCCACCCCGTACGCCGGGGTTGCCGGAGGTTGCCGGCCCGCGGCCC

66424 GACGACCCGGTTCGTGGCGGGTGCCGGCGGAGGTGAGCGCCGCCAGTTACTCCAGTCGGGGGGCCTCGGTGATC

                     <·   E L E H L M L Q R A A E T I

66515 GAGCCCGACAGGCTCGGGTAGATGGTGATGTCTGGGCCAACTCGTTGACCGTGAGGTTGTTCTCCACCGCGTGATGCGGCAGGATCAG

           <S G S L S P Y I I T Q A L E N V T L N N E V A M T I P L I L

66607 CTCGCTGGCCTTCGGTGCCACCACCACGCCGATCACCGGCCGGGCGGAGGCAGAACAGCTTCACGAAGCCGTCGGCGAGGTCGT

          <E S A K P A V V V G G I V Q G S A P R C G L K V F G D A L D D

66699 CCATCTTCGCCCGGGGCGTTGCCCGACAGCGGCATCACCTGGCGGGCCGGGGTCTTGCCGGCGTCCACCTCGTCCTGGGAGACGCCGACG

         <M K A R A N G S L P L M V Q R A P T K G A S V E D Q S V G V

66791 GTGGCCAACTCGGGTCGGTGAAGACGTTCGCCAGCGTACGCAGCCGCCTCGCCGAGCCGTGCCACATCGCGAT

         <T A L E P D T F V N A A V T R L R L P R V A E G L A H W M A I

66883 CCGGCCCTGCATGGCGGCGACGCTGGCCAGCGGCAACACCCCGTGCAGCGTAGATCCGGGGACGTTGGTGCGGGACACCC

         <R G Q M A A V S A L P L V G T C D G A A Y I G P V N T R S V R

66975 GGTCGACGGTGACGTGAGCCGCCCAGTCGACGCGCTACTCGGCGAGGCCGAGGTTGGCGGTGTTGGGGATCGGGATCGAGCGCGACGCGGATG

         <D V T V Y G G R A L E V G T E A L G L N A T N P I S G V A I

67067 AGCGCCGGTGCGAGCCGTGCACCAGCGGCCGGTCCAGTTGCACCTCCACCCCGTCGGCGGATGCGGCCCTCTCGGCGCGCGGGAGTTGTT

         <L A H S G H V L R G D A L E V E V G D A I R Q V R E A R S N N

67159 GAGGATCGTCATGCCCGGGGAGCGGAACACGCGCTCGATCGCGTCGTCGTGCGGCATCACCCGGTCCCGGCTGGAGA

         <L I T M G R S R F V R E I A M A A D A D E H P M V R D R S S V

67251 CGAGGTGACCGGGACCCCATGGCCAGGTACGCCGCCAGGTCAGGTCAGGATCGTCGGCGAACTCGGCCGGCATCAGGTGCTCGGGCAGG

         <L T V P V G M A L Y A S A F E A G T V G S G V V I L H E P L

67343 TGCGGCAGGTCGTACCTGCCGCCAGGTCGTACACCTGCCGCTCCGGCACGCGCTCGGGGGGTGGCGGGGTGGCCGGTGGCCGAC

         <H P L D Y V Q E W T L I R E G D P V A T P L Q R P T A G T A V

FIG.11A(58)

67435 CAGCACGGTCGAGCGCGTCGATCGAGTGCTTCTCGGAGCCGTGGCGCCGGCCGTGGCCGTGACGACGACGCGTGGTGTGGCCCAGCATGTCCTCGCCGA
< L V T S A D I S H K E S G D A P T V V V R H T H G L M D E G L

67527 GCCGGGGCCGTGCCCACGAGAGGTGACGCCGGCTTTCACCAGCTTCGCGTGGATGTCGGCGGACTGGGCCAGGGCGAGCCGCTTGACCGC
< R A T G A V F T V G A K V L K A H I D A S Q A L A L R K V R

67619 TCGTGCACGGCCCGGGCGTCGACGGCGTCCTCCAGCCCGTCGGAGTGCCACCCGGAGTGGTCCGGGTACCGGGTGACCACCTC
<E H V A R A D V T V A E L G D S H V G F E E T D R Y G T V V E

67711 CGAGCTGGGCGGATGAACGTTTCGACGGTACGGCAGTCGGACAGCAGTCGGACACGACGACGGCGACAGGCGGAGAAGAAGTTGTCGACATCAGCGGT
< S S A I F T K S P V C D S L V C A G G A G E A E V V T V D A D

67803 CCAACTGGGCGGCGACCAGGCCGCCTCGTACCCGCCGGCCCCCGCCGATGATCACGATCGGCTCACAGCTATCGCCCCTCGTCCGT
< L Q A A V L A A E Y G A P G G G I I V I Q S V

67893 GCTCACAGTGACTTTCTTCTCCCCGACGCGTCCGACACGCACGCGTCGTATTCCCCCAGCGTCTCATCGTCATCGCCGTGCG
> V R

67984 TCACTACGCCGCCTACGGCTCAAACCTGACCCGCCCCGGATGCGCGCCTACTGCCCGCCCACTCCCGATGGTCGGGCGTCGGCTGCTGGGAGG
> H Y A A Y G S N L D P A R M R A U C P H S P M V G V G W L E

68076 GCTGGGCGGCTCACCTTCGCGGGTGAGGGCGCGATCGGCTGGGAGGCGCGGTCAGCACCATCGTCGAGTCCCCGGTATCGGGTGTTCGTG
>G W R L T F A G E A I G W E G A V S T I V E S P G D R V F V

68168 GCGGCTCTACGACGCCACCCGGTACGACGCCCAGCTCGACGAGATCGAGGGGGTGGCCTCCGGAGGGGTCAGCGGTACCGCAAGCTGCACGTCCGCGT
>A L Y D I H P Y D A V Q L D E I E G V A S G T Y R K L H V R V

68260 CTCCACCCTCGACGGCGGCGACGTGACCGCGTGGGTCTTGACGTCTTGACGGGTACGAGGGGCGGCCTGCCGACGGGTACGGGTGGTATCTGTCGGAGATCG
> S T L D G D V T A W V Y V F D G Y E G G L P T A W Y L S E I

68352 CCAACGCCGCCGAGAAGGCGCGCGCCCCAGACGACTACGTCAGCGAGCTGCGGTCCCGCCCCACCGGCACGGCGTCGGCGTAGCGGCGTCTC
>A N A A E K A G A P D D Y V S E L R S R P T G T A S A .

FIG.11A(59)

68443 CCACACTCCCAGTCTGCTCCGCCCGAGACGGGGCCGCACGGCGGCCCCGCGCGGGGGTGTCGTCTGTCACACATCATGGTCGCGCCCGTCACA
                                                                                              < .   V

68534 CCGCCGTGGCGGCGGGGGGACGGTGCGCTCGTACATGTCGGTCCAGCGCCATCTCGGGCAGCCCACCGAGCGGTAGAGCGGTCGCCGGGGAGGTC
        < A T A A P V T R E Y M D T W R M E R L G V S R Y L T A P S T

68626 GGGTTGGTCAGGTCGACGGCCGGAGGCGGCGGTGCCGCCGCGTGCCCGCGTAGACCGGTGAAGGCCCGCCACAGCAGCCGGCCGCCGACCCC
        < P N T L D V G L G A H R R G K A A Y V T F A R W L L A A G V G

68718 GTGCCGCCGGTACTTCGGCAGCACGACAGGGTCCGCACCCAGCCCGAGTCCTGTTCCAGCGCCTGGTCGGACGACTGCAACGCGCCGGCCG
        < H R R Y K P L V S L T R V W G S D Q W L A Q D S S Q L A G A P

68810 GCTCCCGTCGACCTCGGCGACGAACCACTCGTCCCAGGTCCTGTCGTGTACGGGGCAGACGCTCCGCCCAGTGGTGTACCGCCGGCTCG
        < E G D V E A V F W E D W T R D Y A P L R E R W H D Y G A P E

68902 TAGTCCGGGGTGTCCCGGAACGCCGTGTCGTAGATCCGGTGGAACAGGCGCAGGTCGTCCTGTCGCCGGCGGCCGGACCGGTCAC
        < Y D P T D R F A T D Y I R H F L R L D D E D G A R L P R V T V

68994 CCCGGGTGGGGCGGCGGCTCGGCGGGGCAGCCCGGCGCAGGTCATCCGTACGACTCATCCGCTTCACCCGGCTGAAACCGGCCTCGGTCA
        < G P P P P E A P L G A L D R S M R V Y R K V R S F G A E T L

69086 GCTCCGTCGTCACCCAGCCAGCGGGTCTCCGGCGGGTAGGCGTAGGCCGAGGCGCGGAACGCTCCGCGCTCCGCGCCGCCGACCCGG
        < E T V W R T E P P Y A S A R V T L A P L S R E A A R E A V R

69178 TCCAGCATCAGAGCGAGCAGCGGGGCGGTACCGCCTCGGCGCCTCCGGGTGCGACGAGACGTCGACGAACTCCCGGCCACCCGGTCGG
        < D L M L A L L P A R V A E A R E P D V L V D V F E R G V G T P

69270 GTTGTCCACCACGACCAGCGACGAGCGGCCCTGCGGGTCGGCGTGACGCGCAGGAGTCGCGGCGGTCGAAGAAGGGGCCGTCAGGG
        < N D V V D Q A V L R G Q P D S V L W S D R A P D F F P A T L A

69362 CGGCCCTTGACGTCTTCGGCGTCGAAGTCCGGGTGGCCGATCGGGCTGGCCGTGTCTGCGGCGTCGCGCACGACGTCGTCG
        < A K V D E A D F D P H G I A F T D A A H V V A L I G P V D D

69454 AGGGTGGGCGGCGGCCCAGTCAGCGGGGCGATCCTGGCAGCCACCCGGCGCCGGTCCCGCGCCCTCATTTTCAACCGC
        < L T P R R A A W D A P L T V

FIG.11A(60)

69545 CCCGGGCCCCTGCCCCGCCCCGCCGCTCGCCGGCGAGAGGGGACCCTTTCTACCCCAGGCGTTAGTAAGGGGCCCTTCCTTGCACCAC

＜ ・ Y P A R G Q V V

69637 GGCGCGGTGCGGTGGTCAGCAGGTCGAGCAGCCGGTGCCCTCGGCGCGTGAGCGCCCGGAATCCGGTCGACACCAGCCGGTCGGTCACCG

＜A R A T T L L D L L A T G E A P T L A R F G T S V L R D R V A

69729 CCTCCGACCACAGCCGGCGGCGCCACCAGCGGCCCGGGGGTACGGCGGCCAGGCCGGCGGCAGCCCGGCCCTCCCGGC

＜E S W L R R R V L P G V R P Y P P P W G C A L A G A E G E P

69821 CCGGCCAGCAGCACCGGCCTCCAGCGGCGGTCATCCGGCCCGCCACCGGCCCAGCAGGTACGGCCCGGGGAAGTGCTCCGAAGCAGCAGCCC

＜G A L V A E L P T M G G A R V A L L Y A G A F H E R L L L G

69913 GGGCGGGGGCACGGGGCCCCGGGGGTGTCGTCCGGCGGCCACGGGCCCCAGGCGGCAAAGAGTGGCATCCGGCGTCCGGCGTCGGTCGA

＜A A A R A G P T D D P P P V A R W A A F L P , G S A D A A D V

70005 CCACCCGGTGCAGCAGCGTCGCCAGACGGATCACGCGGGCACGGCGGTCAGGTGCTCGCTCGCCCACCGGCCAGCACTCGGCCAGGTTCGCC

＜V R H L L T A L R I V G P V A T L H E S G W R C C E A L N A

70097 GTGGCCACCTCCAGCGAGGCGTGCACCGGAGGCGGCGGGGGCGGGGGCGGCGTCCACCGTCGGGGGGGCGACGAAGCCGAGGGCCGCGCTCAC

＜T A V E L P A H V R A A A D W G S A V A D P A V F G L A A S V

70189 CGTGGCGGGCCCCGACGTCGCGGCAACATCTCCCCGAGCTCCAGCACCAACGGCTTGCTCGCGGCGGCGACCTGCTCCGGCGTCATCGGGTTCAGTCT

＜T A A G V D G L V G A R G A I H F A Q G S I G L L R A R H L T

70281 TGGCCGGGCAGCGGCGAACATCTCCCCGAGCTCTTCGGCGTCTTGCGACAGCCCCGTCTTCGGCGTGCCGGCGGCGGT

＜ A P C R A F M E G L E L V L P K S A A A V Q E P T M ＜・ D

70372 GCCCCCGCCCGGGGCCCTTCCGTGACAGCCCCTCTTCGGCGTGCGACCCCCTCGATTTCGCCGGTGCGGCTGGGCGGCGGGT

＜A G G P G E T V A G D E A D V A E I A G E I E G T R R Q A A T

70464 GACGGCCCGTTCCGCCGCCGCCGGCCAGCTTCCGCCGCCAGGTTCCTGCTCGCGCGGCCTTCTGCGCCGCGATCGCTCGGCCAGCGACC

＜V A R E A A R R A L K R R S L E Q E A E A R S R E L E A L S R

FIG.11A(61)

70556 GCTCGATGCCGGTCAGTTCCTCGGCACGGTGCTGTCGGCCTCCACCGGCGCCGGCAGCTCCGCCTCCTGGTCGGTACGCGCC
< E I G T L E E A G D H E A E V A G A L E A E R E Q D T R A

70648 CGGCGCCAGTTCCGGTTCCAGCATCCGGCGTTGCCGGCCCGCTCGGCCGCACGGACCGCGCCGCTTCCGGCGCGGG
<R A L E R E L M R R Q R A R E A R A R E A R A A R E A R K A R P

70740 TGGTGGGTGGGGCGGTGGCGTGCTCCTCGCCGGTGACCAAACGGAGCTGGGGGCGGGCACCTGCCGAAGCGGTAGCTGGCGG
<P P H T P P Q E E G G T V L R L Q P R P V E G F G A Y S A A

70832 CCCGGCAGCAGCCGGCGGCACGCCGGAGCCGGCCACCTGCCCGGCCCGCTCGAGGAGCGGGGGCGTCGCCTCCAGCGGCCAGC
< R L L R G S R V Q G A V E T D S L A A D L T A E V E G L P L

70924 TTCCCCGGCCGGGGCGGCCCTCGGCGTCGTGTCCCGGCCAGCCGCCGCCTCGGCGCCGCTCGGGGCGCTGGGGGGAGAG
<K G A P P G G E A D A A L R R A E A V L A A V A A R R Q A S L

71016 TTCCCGCAGCCGGGGCGCGCCAGTCGCGCCTGGGCGCCTGGGCGCAGTTGGGTCAGCTGCGGCGGCGGCGGCA
<E R L R P G R L D R Q A R R L A E A L Q T L D A V L E P R R L

71108 GGGCGAGCAGGTTGACCAGCGCGCGCACGCGGGCCGATCTCGGGGGCGGCGCCGGGGCC
< A L L N V L W A A V T P R R L R A I E R A T A P D G S R R A

71200 TCGGCGGACGGCGGCGTCGGGTGGCGACGAACTTCTCCGGCCCTGCGGGGGCGGCACGGCTC
<E A V A A D R T A V F K E P P E T Y L R R L L S Q P P P V < .

71291 AGACGTCGAGCGGGCTGCCCGGCTCGAGGGCTGGTAGTCGGTCCCCGACAGCGGCGTACTGACGGTTGAGGACGGCGAGGCCGTTGTCG
< V D L R S G P 0 E L R Q U D T G S L A A Y Q R N L V A L G N D

71383 TTGAGCAGCCGCTGTGCAGGGCGGCGAAAGGCTCGGCGCGCGGCGACCGCGGATGAAGTCGAGCACCTCGGAGAACTTCGACCAGGGGCGTG
<N L L G D H L A F A R R P A V A R I F D L V E S F K S W P A H

71475 GATCGGCGGCGAAGAGGGGTGTCCACGGGGGGCGTCCTGGGTGCCACCAGGGCGTCGGGGGTGGTAGACGACGTCGTTCAGCAGATACCCGA
<I P A F L T D V P A D E P A V L A D G P H Y V V D N L L Y G L

FIG.11A(62)

71567 GGTTGTCCACGACCGGGATGTCGGGATGGATGACGGGCGGTGCCGACCGGCCAGCCCGCCCGCGGTGAACGCCTGCCCG
      < N D V V P I D P H I V A H R G G Y A R V A V G A A T F A Q G

71659 GGTGAGAGATGGGGCTTCCAGGGCTTCGGCCACGTCGCCGAGGGCACCGGCCGGCCGTAGATGCGGAACGGCCAGCGGTG
      < P S I P E L A E A V D G L A G A L S A P G Y I R F P W R D L Q

71751 CCGGGTGAGAGCCGCGACGTCCACGTGGTCGGGGTGCTCATGGGTGATCAGCACGCGTCCAGCGCGGTCGGGTCGCTGAAGA
      < R T L A A V D V H D P H E H T I L V A D A G D L A T P D S F V

71843 CGCCCGGGTCGACGACGACCAGCACACGCCGTCGTGCTGCGACGCGGAGGCAGGAGTGGGGCAGGATGGTGAGCTGCATCGTGAT
      < G P D V V L V G G D H E V R L C S H A F K T L Q M

71933 TGACCCAATCGTGATGTCCCTCAGCGCAGTCTGCCGAACCGGCTCGCCGTCTCGAGGTATCGCCCGATGGGGGTAGACGAT
      > M R V R V

72025 CGGAGCGGGGAATGGACGACGCAAGAGACGCAGGTTGCTGACGCGGTGGGGCTGGTTGCAGCGGCCGGACA

72117 GCGATGGGGCGGGGAGAGCCTTCGGCGGCGGTGGCGGCGCACCTGCCGCGAGCGGCAAGGCGGAGCAGGGTGCCGATGCCGGG

72209 GGAACGCGGGTCCGGGCGGTGGCGGGGCTCACCGGAACCATCGGGGTGCGGGGTGG
      > M R V R V

72300 ACGATGTGGACGCGCCGGGCCCGGTCCGCCATCACGGCCGTCGGCGGGCTTCGTCGGCGGCGACGAGCGCAGCAGCGGCGGAACC
      > D D V D A A A R S A I T A V T G V G G F V G G G D E R S S G G T

72392 GCCGACGCCCGGGCGGGAGTTGCAACTGCCGGGTGCCGGGCGGTTCACGGGCGTCCTGGAGGAGTTGGCGGAGGTCGGCCGGCAGGAGCA
      > A D A R A E L Q L R V P A E R F T A V L E E L A R L G R Q E Q

72484 GCGGGGCGGATCCGCAACGCGGACGACCGGTGACGAGGAGACCGTGACAGTCTGCAGGCGCGGCGATCGACGCGCGCGCGGGCGTCGGA
      > R A I R T E D V T E E T V D L D A R I A T Q R A R V E S G R

72576 AGCTGCTGGCCCGCGGCCGACCTCGATCGGCGACCTGGTGACGCTGGAGAGCGGGGAGGTGGCTAGGCGGGAGGCCGACCTCGCCTCGCTGGAGGCG
      > K L A R A T S I G D L V T L E S E V A R R E A D L A S L E A

72668 AAGAAGCGGCGGCTGGCCGACCTGACCTCGCTCTCCACCATCACCCTGACCCTGCTGGTCCGGAGCCCGGACACCGAGCCCGA
      > K K R R L A D L T S L S T I T L T L L V G P E A E A R D T E P D

72760 CACCGGCTTCGTCGGGCTGCGGCGGCGGCTGGGTGGCTGGACGGCGTTCGTCGCCTCGCTGGGCGTGCTGCTCACCGTGCTGCTGGGCGCGCTGCTGCCGT
      > T G F V V G L R G G G W T A F V A S L G V L L T V L L G A L L P

FIG.11A(63)

72852 TCGGGTGGCCCTCGGCGGTGCCGGTGGCCGGTGGTCGTGCTGGCGGTGGCGGCCGGCGTCGACGCCGCGGCCGGCGTCAACGCGCC
>F A V A L G V P V A V L L A V L R R R R P P A A V N A P
                                                        < · R A

72943 GCCGGCCAGTGCCCGGCCAGGCGGTCTGCACCATGACCGGATGCCGACCGGATGCCGTGCAGGT
> P P V P A A R S A P ·
<A A L A R L A T Q V M V R I G V A I A G E D V D F S A R H L D

73034 CGACGTTCGGGCCGGACCGGCCGACGGCCGAGGCGGGCCAGGCGGGCCAGGTACCAGGAGAAGTCCTCGCCGCCATGCTC
< V N P G S R G V G L R A L A G P V Y E L Y W S F D E G G M S

73126 TGCGGGGTCTCCGCGACCCCTCCGGGCGTGGGTCGCCGCGAGCACGTGGTCGTTGGTCACCGGCGG
<Q P T E A V G E P G L A A H T A A T L V Q I A R A D N T V P P

73218 CCGGCCGCGTAGGTACTCCAGGTCGACGTGGCGCCGGTGGCGGCGGCGGATCTTGGGGGCCTGGTCCC
< R G R L Y E L D V T A G T P A I V D R V V Q A V I K P A Q D W

73310 AGGTGTCGGCGGTCCATCACCGCCAGGGTGCCGGACGCGCCTCGGACGCGGGGACCGGAGGCGGTGGCCGAAC
< T D R D M V R L T G S A S A E S P I V N Y R T G A S A H G F

73402 ACGAGCAGCAGCCCGCTGTTGGCCGGCGAGGCTGGCACCTGGTGACCAGGCGGACCAGGTCGAC
<V L L L G S N A P V R R S V L A P V E T V L R G L A D V L D V

73494 GGTCAGGTGCGCGAGCGGGTGTGCCCCGGGCCGGTGAGCCGGACGGTGATCGGGCCGACCCGCAGGC
< T L H P R A T H G G P G T L R V T V N D A A A T I P G V E L G

73586 CGACCTTGCGCACGACTCGCCGGTCGGGGTCGCAGTGCAGTGACGAGATCTGCACGACGTCGTCGTCGAGACGGAG
< V K G V P Q N P D V H L A F I Q V V D D L G G A E I V E L S

73678 CCGGCAGGGCAGGATCTCCTCGGCCGGCTGGAAGATCAGCCGGACCCGGTCCAATTCGCCGAGGTTGGGCGAGTTGGGCCAGCAGCACGCC
<G C P L I E E A P Q F I L R V R G D L E G L N A L Q A L L V G

73770 GACGCCGAGCAGCAGACGACGGTGGTGCCGCAGTCGTGGCCGCGCCCGAGGCAGTCCTTGGTGGACCACGTCCTTGACGTCGG
<V G L L V T T H V D H G C A H C V G D K T S R Y P V D K V V D T

FIG.11A(64)

73862 TCAGGGGCCAGAGGCGGTCGATGTCGGGGGCGGGGGAGGCGGACCACCGGGGCGGTGGGGGGCGGCCGTGTCGATGTCGCAGATGACCCGTTGCCCTTTGGC
< L P L A D I D A R L A V V P G D P R G D I C I V G N G K P

73954 AGCAGGGCGCGGGGCGCAACCCGGCGAGCGAGCGACAGCTCGCGGGCGTCCGGGTGGGGAGTG
<L R P R L G A L S L E R A I L A A T E F E E G S L E P H S H

74046 GATGTGCCGCGGGGTGGCGATAAGGCCGGGCATCCGGAGGGCGAGCAGATGGTGAGCTCGAAGGCTGCCAAAGGCTGCCGGACGCGGCGACT
<I H R R T A I L G P M R L A L L H D L E F P L P Q S G S P S E

74138 CCGGCCAGGCCGACGACGCCAGGTGGCTGCCGTTCGGCGAGCGTCAACGCACTCGTCACGTGAAATCTGATCACTAGAAACGGATGGATC
< P W A S S A L H S G N P L T L A S T V

74229 ATCAGGGGATGACAGCCGCCAGCCTTCGACGGTGACTCGTGCAACATCATTCCGTAGCGATCGGAACGCGCAGCGGTCACGAATAC

74321 CCTGGTGGAAAGGGCTCCATAATCTGCGGGACAGCAGGTAGATCGGCGGTTGAACGCGTCATCTGCCCCACCTCTACAACCGTAACCGA

74413 TTCGGCGGTCACGAAATCACCGTCGATCCGGGGCCGTCGCTACCGAATTGTCGCATTAGTCGTCTGGTTAACTGCCGTCTGGACAAGTAAC

74505 CGACCGCCACTCGGCAGTCGGACGACTCCCGACGGTGACACGACGGGCCGACCTGTCTCCGTCCAATCACCCGGACGGGG

74597 TTACCCACTGCCCCGGGTGGCACACACCGGGCTGCCCGGGGTGGCCACAGACCTGCCCGGACCC

74689 CTCATCCGAGACAAGGGGTCAGAACCGGTCGTCGGGGGGGTACGTCCCCCACCTGGGGGCGGTGCCACAGACCTGCCCGGACCC
< . F R D S P R Y T G W V Q R L T G C V E G V T A

74780 CGGGCCCGCGCAGCCGCCTCCTTCATCGGGTGCAGCACGTTCGCCGTACCCTCGGCGGCGGCCGCCGCTCACCCAGCGCGCGCTCGACGGCGTC
<R A R L A E K M P H L V N A T G E A A A R L E G L A R E V A D

74872 GCTGTGCGCGTCCACTCGGCCTTGGCCGAGCTTCGCGCTCGGCGTGGGTCCAGCCGCAGCGGCTCGTGCTGCGGCTCGTCGG
<S D R E V R L K A L R E A Q A A E I T P D V R L P E Y P E D A

74964 CGTGACCGTGAACCGGTTGAGGCGGACCACACCCGCTCCGCCGAGTCGATCTCTGGGCGATCGGTACGGCGGACTGCTCGATCTCCGC
< D V T F R N L G V V V R E G S D I E Q A I R Y A S Q E I E R

75056 TTCTGGAAGCCGGCCTCGACTGGTCGGCTGACCGCGTCGGCGGAGCCGTCCACCACCGCGCTCCATCAGCTCCACCACCGCGCCTCGATCTCGGCGGT
<K Q F G A E I A D V V S G H D A V R E M L E V V A A E I E A T

FIG.11A(65)

75148 CATCGCCTCCACCACGTACGACCCGGGCGAACGGGTCGACGGTGGCGGTCAGGTCCGTCTCGTACGCGAGCACTGCTGGGTGCGCCAGCGCCA
<M A E V V Y S G A F P D V T A T L D T E Y A L V Q Q T R L A L

75240 GCCGGGGCGGCCTTCTCGGTGGGCAGCGCGATGGCCTCGTCGAAGCTGTTCGTGTGTAGCAGCTGGGTGCGCGCGCACCGCGCCCAGCCCC
<R A A K E T P L A I A E D F S N T H L S Q T G G L V A G L G

75332 TGGATCGCCACCGACCAGGTTCACCTCGGGCGTGCTGGGCCGTGAGCTGCACGCCCGTCTGGGTGTGGAAGCGCAGCATCATCGACTT
<Q I A V R V L N V E P Q Q A T L Q V G A T Q T H F R L M M S K

75424 CGGGTTCTTCGCGCCGAACTCGTCGCGCATCAGCCGGGCCCAGATCGCCGGGCGGCACTTCGGCGACCTCCTCCAGCAGGGTGGTCC
<P N K A G F E D R M L R A Q I R R A A R F K A V E E L L T T R

75516 GGGCGACGGAGAAGAAGACAGCCCGGGGCGAAGTCGTCCACGCGCTGCGCGGCCATGTGCTCGGCCGCGCTGGGCTGCTCGATGGCC
< A V F F F S L R P A F D D V A L G A A L A A R V Y E V G N A

75608 AGCGTGAACGCGATCTCCTGCGCGGGCGACGCGCCCGGCCTCGGCGATGTGGTAGCCGGAGATGGAGATGGTGTTCCACTTCGGCCACCTCCGC
<L T F A I E Q A P S A G A E A M H Y G S I S I T N W K P V E A

75700 CCGGCAGTAGGCGAACGTGTCGGCGGAACAGCGCCAGCCAGCGAGGGCTTCGGCGGGAAGATGTACGTGCCCGGGCGATGTACTCCTTGAGGATGT
<R C Y A F T S A V L R L S P K P P F I Y T G R A I Y E K L I D

75792 CGTTCTGGATGGTGCCGTTGAGCGCCGGTGAGGCCCACCCCGGCCTCCTCGGCCGAGCTGGTAGAGCCAGCAGCACCGACCCCGGGGCCG
<N Q I T G N L A A G P V G A E E A V L Q Y L L L V S G P A

75884 TTGATCGTCATCGAGGTGGAAACCTTGTCCAACGGGATGCCGTGGAACAGCAGCCGCATGTCCTCGAGTCGATGGCGACGCCGACCTT
<N I T M S T S V K D L P I G H F L L R M D E I S D I A V G V K

75976 GCCGACCTCGCGCTGGGCGATCGGGTCGTTGCCGAGTCGTACCCCATCTGGGTGGGCAGATCAAAAGGACGGAGAGGCCCATGGTGCCGGCGC
<G V E G H A I P D D S D Y G M Q T P L D F A V S L G M T G A R

76068 GCAGGAGCTGGTGGTAGCGCGTTGCTCTCGTCGTGGTAGCGGCGAAGCCGGCATCGTCCACGGCCGCGAGGTGTACATGGTG
<L L Q H Y R A N S E T A T G F G A Y Q R M T W P R S T Y M T

76160 GAGTAGACCCCACGGGGTGTACGGGTGTCCCCGGGAACTCCCGGCGTCCCTCGGGCAGGTCCCTCTGGGTGTGTAGACACCCTT
<S Y V G R T Y P F F E G P E G L R E E P L G E P L D R Q T Y V G K

FIG.11A(66)

76252 GATCGGGAAGCCGGACTCGCTCGACCGCGGTTCACTCATCCCGGATGGTAGGACGTGCCACGCGCCGGAGGGTGAGGGATTGCGCACAT
<I P F G S E S S R P E S M

76343 CGCACCCCTGTCTTTCCCGCCGACTCCGAGGGTGAACACCTGGCCACGTTCCGCCCGTCGGGTTTCGCA

76435 TCGGGGCGTCGGAACCAGCAAGATAGAGGAGTTGTGTCCCAGCACCGCCGCCCCCTGATTTCCCCGGTGGCTCTTCTGTGACTCAGATCCCGACGTGGA

76527 GCGGGCGACCAGTCAGCCACCACCCACGACGTGCGGCAACGTGCCACCACCATCGGTGACGCCTCCGGTACTCGCTCCGGTGGGCAATGGC

76619 GGCATGGGCACGGTCTGGCGTGCCACAGACACCCTGCTGCGGCGGGACGTGGCGGTGAAGGAGGTCGTCCTCCCGCCGGGCCTCGCCCCGA
> M G T V W R A T D T L L R R D V A V K E V V L P P G L A P

76710 GCGACCGCGACGCCATGTACGAACGCACGCTGCGCGAGGCCGCGGCCATCCAGCACCCGGCCGTGGTCCAGGTGTACGACGTG
>S D R D A M Y E R T L R E A A A A I Q H P A V V Q V Y S V

76802 GTCACCGAGGGTCGCCCCTGGATCGTGATGGAGCTGCTGGACGCCCTGGCTGACATGGTGATCGAGGACGGGCCGGTGGCCCC
> V T E G G R P W I V M E L L D A R S L A D M V I E D G P V A P

76894 CCGCGCGGTGCCAAGATCGGCATCGCCCTGCTCGGCGCGCTGGAGGTGGCCCACGCGGGTGTGCACGCGGTGAAGCCGGCCA
> R A V A K I G I A L L G A L E V A H A I G V L H R D V K P A

76986 ACGTGCTGATCTGCACCGACGGCCGGTGTGCTGACCGACTTCGGGGTGGCCAAGCTCCCCACGACGTCACCACGCCGGGGATG
>N V L I C T D G R C V L T D F G V A K L P T D V Q L T T P G M

77078 GTGCTCGGCTCGCCGCACTTCATCTCCCCGAGCGGGCCAGGGGCCAGGAGTTCGGCCCGCCGAGCGACCTGTTCTCCCTCGGCGTCACGCT
> V L G S P H F I S P E R A M G Q E F G P P S D L F S L G V T L

77170 CTACACGGCGGTGGAGGGCCGGCCGCCCCGTTCGACAGGGGCGACCCGATCGAGACCATGCACGCCGTGGTCGAGGACCCGCCACGCGCCGC
> Y T A V E G R P P F D R G D P I E T M H A V V E D P P A T P

77262 AGCGCAGCGGCCCGCTCACCCGCGTGCTGATGGGGCTGCTGGAGAAGGACCCGGCCCGCCGCCGACTCGACGTGCACACCGCGCGCGATGCTC
>Q R S G P L T R V L M G L L E K D P A R R L D V H T A R A M L

77354 CGCGAGCTGCTCGCCGGCCCGCTGACCAGCACCGCCACCGCCGTCAACTCGGTCACGGACCCGTACGCGGTGCCGGTGCGGTGCAAGCAGCGGCCC
>R E L L A G P L T S T A T A V N S V T D P Y A V V P V K Q R P

FIG.11A(67)

77446 GGCCGTTGCGCCCCACCGCCCTCCGCTGCGGAGCCGAAGCCGGGGCAGATCGGCGGCCGGGGCGATGCTCGCCCCCGGCGAGTGCTGACCG
> A V A P P P S A A E P K P S G Q I G G R A M L A P G E S L T

77538 ACCGGCTGGCGGCCCTGCGCGGGGGCGAGAAGACGAGGAAGAGACGACGCCGCCGCTGGACGACACCAGCGCCGACGCGCTT
>D R L A A L R R G E K T R K T T T A A A L D D T S A D A L

77630 GCCGGCCCGCTGCACACCCCGACGGGGGCGATGCCCGCGCCCCGCCGGAGCGGTTCGTGGAGGCCACCCAGCGCGGGT
> A G P L H T P T G A M P A P P P A G R T Y G G S S E A T Q R V

77722 CGACGCGGGGGACCGCGCCGGGGAGGCCACCCAGCCCGGATGACGTACGGGCCCGACGCCCGCCACCCAGCGGGTGTCCCAGGGGAGCGGGCCCGT
> D A G T A P E A T Q R M T Y G S P P D A T Q R V S H G S G P

77814 CGGAGGCCACCCAGCGGGTGCCCTACGGTGGCGGCTCGGCCGACGCGCAGGTGCCCTTCGGTCGCCGGCCAGCGGGCGACGCAGCGG
>S E A T Q R V P Y G G G S A D A T Q Q V P F G R R P D A T Q R

77906 GTCCCCTACGGCAGCCAGCCCGGCACCGGTCCCGGCTTCGGGCGACGCGACAGCCAGCCCGGCGTCGGCGGCGTACGG
> V P Y G S Q P G A T Q P V P G F G A S P D A T Q R V G G A Y G

77998 CGGCGGCCAGTGGTCGGTGCCGGGCACCGGCCAGCCGTGGGCCACCCCGGCCACCGCCCCGGCCACAGCGCCGGGGGGGTCG
> G G Q W S V P G T G Q P W A T P A T A P A P A T A G G G G V

78090 GCCGGCCTCGTCGCCACGGTCAAGGGCTGGCCGCGCAAGGTGCAGCTGCCGGCGGTCGCTGCTGATCGGCGTGTTC
>G R L V A T V K G W P R K V Q L A A A G G V A V L L L I G V F

78182 GCCCTCTTCGGCGGCGACGACCCGGAGCAGCCGACCACCCCGCAGGGGCCCGCCGGGGTGGAGATGCA
> A L F G G D D P E Q P T T P Q G P S A G A P A G P G V E M Q

78274 GGAGCAGTCGGCCAAGGGCGTGACGGTCCAGGTGCAGCCGAAGGGCTGGGAGCGGCGCAGTGCCGACTACATCGATC
> E Q S A K G V T V Q V Q P K G W E R R S A D G G V W V D Y I D

78366 CGGAGGACAACAGCCGCAAGTGCGCATCCTGCCGAGCGGGTGAGCGGTGGAGCGGTCACGTCGACTCGACGAGGCTGCGG
>P E D N S R K V R I L A E R W S G T S T R W A E T A A N G L R

78458 ACCCGGTCGGCCTCCTGCCAGAAGCGTACAACCAGGTGTCGATGACCGAGCAGGAGCTCGACGGCAAGGCGGCGGAGTTCGAGTACAC
>T R S A S C Q K P Y N Q V S M T E Q E L D G K A A A E F E Y T

FIG.11A(68)

78550 CTGCGGGCGACGGGCGAGGGCAAGCGGCACGGGCGTGTGGCGCGGGGTGGTGTGCACGAGAGGGCAAGGTCTACTGTTCTACCTCTCCTGCGACGGACG
> C G D G E G K R H G V W R G V V H E G K V Y S F Y L S S T D

78642 CCCGGCTTCGCCGAGAGCAAGCCGATCTTCGATCAGATGGTGGCGTCGTTCAAGCTCCGCGGGAGCGACTGAGCCGGGCCGGGGGCCGACGC
>A R F A E S K P I F D Q M V A S F K L R G S D .

78733 GACGGCGCCGGGCGGGGCGACGCGGGCGACGTGGTGAGCGCGGTGCTATCAAGAGCCATGGCGGACACCACTGACCTCGACGACACG
> M A A D T T D L D D T

78824 CGCGATCTGGACGACCTTCGCGACCGGGCCGGCGTGGCTCGACGAGACCCGGCCACCCGCGACGAGCTGGAGGCCGTGGTCGA
> R D L D D L R D R A R R W L D D D P D P A T R D E L E A V L D

78916 CGGGCTGCCGGCGAGCGCGGCGGAGCTGGCCGACCGGTTCGCGGGCCCACTGACCTTCGGCACCGCGGGCCTGCGCGGCCCGCGGGCCG
> G L P A S A A E L A D R F A G P L T F G T A G L R G P L R A

79008 GCCCCAACGGGATGAACCTCGCCGTGGTCACCCAGGCCGCGGCCGGGCTCGTCGCCGGGGCTGGTCACCCAGGCCACCGGGCCGCTGGTC
>G P N G M N L A V V T Q A A A G L V A W L A A Q D A T G P L V

79100 ATCGGGTACGACGCCCCGGCACGGCTCGCGGGAGTTCGCCGAGCGCACCGCCCAGGTGGCCACCGGGGCGCGGCGCTGCTGCTGCCG
> I G Y D A R H G S R E F A E R T A Q V A T G A G R P A L L L P

79192 CCGCCCGCTGCCACCCCGTGCTGGCCGTACGGCGTGCGGCAGCTCGACGCGGCCGCGGCTGATGGTGACGCCAGCCACAACCCGCCCC
> R P L P T P V L A Y A V R Q L D A A A G V M V T A S H N P P

79284 AGGACAACGGCTACAAGGTCTACCTCGGCGCGCAGCTCGGCGGCGAGCTGGGCGCGGGGGCGCAGATCGTGCCGCCGGACACGGCATC
>Q D N G Y K V Y L G A Q L G G E L G A G A Q I V P P A D T G I

79284 AGGACAACGGCTACAAGGTCTACCTCGGCGCGCAGCTCGGCGGCGAGCTGGGCGCGGGGGCGCAGATCGTGCCGCCGGACACGGCATC
>Q D N G Y K V Y L G A Q L G G E L G A G A Q I V P P A D T G I

79376 GAGGCCGCCATCCGGGCGGGGGTCGGCCGCTGGCCCGACGTACCGTCGGCCGGTGCCCGGGCCCGGGCTGGGCGACGTGGTCGTGTCGTACGT
> E A A I R A V G P L A D V P L G P A G Q V V G D D V V V S Y V

79468 CGACCGGGGCCGCCGCCGTGGTCGACCCGGCGGGGCCCGGAGCCTGAAGGTGGCCTACACGCCGCTGCACGGCGTGGGCGCGGCCGTGCTGA
> D R A A A V V D P A G P R S L K V A Y T P L H G V G A A V L

FIG.11A(69)

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79560  CCGCCGCCTTCGCCCGCCGCCGGCTTCGGCATCCCCGGCGTTGGTGTCGCCGAGCAGGGTGCCGGACCCGGACTTCCGGACGCGTCAGCTTCCCC
       >T  A  A  F  A  R  A  G  F  G  I  P  G  V  V  P  E  Q  A  V  P  D  P  D  F  R  T  V  S  F  P

79652  AACCCGGAGGAGCCGGGGGGCGGTGGCCGGTGACCTCCTCGTCGCGCTGGCGCTCGCCGAGCGCACCGGCGCCGACCTGGCCATCGCCAACGACCCCGACGCGGA
       >N  P  E  E  P  G  A  V  D  L  L  V  A  L  A  E  R  T  G  A  D  L  A  I  A  N  D  P  D  A  D

79744  CCGCTGCGCGGTGGCCGTCCGCGACGGCCGGGGCCGGCCCGGCGCGGGGGCGGGGCGCCGGCTGGGGGGGGCGGCGCTGGGCGGATGTGCGCGGGGGACGAGGTGG
       >  R  C  A  V  A  V  R  D  G  R  A  A  G  P  A  P  V  S  G  G  A  W  R  M  L  R  G  D  E  V

79836  GGGCGGCTGCTCGCCGACCATCTCATGCGCCGTGGCCGTCCACGCCGTCCTGCTCCTGCTCGTCGTCCTGCTACGGGCCATGTGC
       >G  A  L  L  A  D  H  L  M  R  R  G  V  H  G  L  Y  A  T  T  I  V  S  S  L  L  R  A  M  C

79928  GCCGCCCGTGGCCTGCCGTACGACGAGACGCTGACCGGCTTCAAGTGGATCGTCCGGGCCGGCGGACCGCTGGGTGAGGCCGGCTCCGA
       >A  A  R  G  L  P  Y  D  E  T  L  T  G  F  K  W  I  V  R  A  G  G  G  P  L  G  E  A  G  S  D

80020  CCCGGCTGGTCTTCGGCTACGAGGAGGCGCTGGGCTACTGCGTCCCCGAGCACGTCCGCGACAAGGACGCGCATCACCGCCGGCTGACCG
       >  P  L  V  F  G  Y  E  E  A  L  G  Y  C  V  A  P  E  H  V  R  D  K  D  G  I  T  A  A  L  T

80112  TCGCCGAGCTGGCCGCCGGGCTGAAGGCGCAGGGGCGCCACCCTCACCGACCGGCTCGACGAGCTGGCCGCGAGTTCGGCGTGCACCACACC
       >V  A  E  L  A  A  G  L  K  A  Q  G  P  T  L  T  D  R  L  D  E  L  A  A  E  F  G  V  H  H  T

80204  GACCAACTCTCGGTGCGGGTGGACGACCTGCGCATCATCGCCGACGCGATGGCCCGGGTCCGGGGCGCCACCCCGTGCTGCTCGGCCG
       >D  Q  L  S  V  R  V  D  D  L  R  I  I  A  D  A  M  A  R  V  R  A  A  T  P  T  T  L  L  G  R

80296  CCCGGGTGACCGAGGCGCGGGGACCTGCTCCCCGAGGCGGGACGTGGTGATCCTGCGCACCGACGGGGCACGGGGTGGTGATCCGCCCGTCGGGCA
       >  P  V  T  E  A  R  D  L  L  P  E  A  D  V  V  I  L  R  T  D  G  A  R  V  V  I  R  P  S  G

80388  CCGAGCCGAAGCTCAAGGCGTACCTGGAGGTGGTGGAGCCGGTGGCGGACGGCGACGTGCCGGCCGCGGCGGCGGCCSCGCTG
       >T  E  P  K  L  K  A  Y  L  E  V  V  E  P  V  A  D  G  D  V  P  A  A  R  T  R  A  A  A  T  L

80480  GCGGCACTCCGCACGGAAATCGCCGCCCTGGTCGCAGGATGGGGATGAGGTGTGCTCCGCCGCTCTCTCAGCGGGTTGGCGTGTCGCCCC
       >A  A  L  R  T  E  I  A  A  L  V  Q  G  .

80571  CAGGTTCGTCGTGGTGATATGCGCCCAGTAAGCCACCGTCCTGCCACTATCCATGTCGTAGAACATGATGCGTGCCACTTGGATGTAGTAGTAG
80663  GTGACCAATGAGGTGAACCCGGGGCCCCTGTTTGAGCGTGTTACGTAGGCGCCGAAGCCACTGGCAGTCACATCGTCACGGCGGGCTTTCCCGTT
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FIG.11A(70)

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80755  AGCGCTCGCGTAGCTCAGCGCAGCAGGAACATCCTCCCGCCATAGGATACAGCAGCTGGCTGGAGCCGTGGTGTATCCTTCTGAAGGGCTTTGCAG

80847  GTTCTGCGGCCAAGGGCGAGAGGGCGAGAGGTCCTGGGCCTCCTCGTCTCGGTGTTGTACGCCAGG

80939  ATGACCGGCACCGGCAAGGGTGTTTGGGAGGGTGACCGAAATGGACGTGAACCCGGGTCCGGGGCGCTGCGTCGGGCCGCTGCCGGCTTGGGT

81031  GGCGGGCCGTCGGAGGAATAACTACGGAACATGCAACAGCCACTGCCGCTTTCCACCCTCGCCGT

81123  TCACCTCGAAGGGCGCTACGGACGACCATCCAGCGCCCAGTGTTGTCCTTCTGGCCATCGAGGCGTAGAGCGCTGGCAACCGTCTTCGTTG

81215  TCCACAACCTGCCACACGGGCGCTGTTGCCGCAGCGGGAGGCATCGTAGAGCTGGACATGACCGCCTGTCTTGTTCTGCAGCGGGAACGACGGAGGT

81307  CCACCCCTTCCGAAATTGCGCTGCCAGCGGGGAGGCCACTCGGGTGGCATCTCGTGTGGCGCCGTGCCGT

81399  CATTGCTGTTGTAGAACAGCACCGCTGGGCCACTGTAGTGCCCGTCGAAATGCAGAGATATGACGTGCGTGAACCCTGGTCCGAGTTGGACA

81491  TCATAGAGAGCATTCCGGAGTGACATGGGTTTACCCGTCCACTGACTGCTTCTCAACAGATCATCAAGGTGTGCGGGCTGCA

81583  CAATCGGGTGGAAGAAGAGCCAGCACCGGGCCTCACTGGCCATCACAGTATCGTCTTCGACCTCTTCGACGTGCGGGGCGAAACGGGCGAACCGAG

81675  AGCGGTTCCGGCGCATCTGTCGGGTCGTGTCGAAGGTGCGGGTGCCCTCCGCGCCGTCACGGGT

81767  TCTGCCACGAGGGCGGCCAGGACCCAGAGACGGTGGCCGGGGAACGCGGCACGCTCACCCCGCGTGATCCCTTGCCACGAAGGGCTCGTGCGCCGCTC

81859  CGGCGGCCCTCCGCGCCGGAACGCGGGAACGGGATTCGCTTCTTCGACGTGCTGGCTGCGCCGCTC

81951  CAGGCCCCCACCATTACCCGGCACCATTGGCATTCGCTTCTTCGGGCGTTGCATTTCCGGCGGAAAGGTGT

82043  TGCACGGTGCGTGAAACAAATGGCTGACGGTGCCGACGGTGCTCGGCGAGCTGCTCACCCAGCTCCGCGAGAGCGCCCATATCAGCA
       >V  P  R  R  Q  L  G  R  L  L  T  Q  L  R  E  S  A  H  I  S

82134  TCGACGCGGCGGCGGGCGAGCTGGACTGCTCGCGGCAGAAGCTCTGGCGGGATCGGGCAGGAGCTCGACCTCGGCCAAGACACCGGACGTCCGG
       >I  D  A  A  A  G  E  L  D  C  S  R  Q  K  L  W  R  I  E  R  G  L  T  S  A  K  T  P  D  V  R

82226  GTGCTCTGCGAGCTGTACCGGGCCACGCCCGACCAGGCGAGCGTGCTGCTCGGGCTCGCCGAGGTGAGCCGGGCCGAGGGGTGGTGGCACGC
       >V  L  C  E  L  Y  R  A  T  P  D  Q  A  S  V  L  L  G  L  A  E  V  S  R  A  E  G  W  W  H  A

82318  CCACGGCAGCTCCGTGCCGGCCTGGTTCTCGCTCTACGTCGGCCTCGAGAACGTCGGCCAGCATTCGGCACTACAACGCGGAGCTGGTGC
       >H  G  S  S  V  P  A  W  F  S  L  Y  V  G  L  E  N  V  A  S  S  I  R  H  Y  N  A  E  L  V

82410  CGGGGCTGTTGCAGACCCCGGCTACGCCGCCACCGGTGGGCGAGGAGCGGAAAGAAGAGCGGTGGGC
       >P  G  L  L  Q  R  P  G  Y  A  T  A  L  F  E  H  N  R  P  E  L  G  E  E  E  R  K  K  A  V  G
```

FIG.11A(71)

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82502 TTCCGGACTCAGGGCGAGGGGCTGCTGGCCCGGGCGGCCCCCGAGCTGACCGTGATCCTCAGCGAGGCGGTGCTGCGCCGGCCC
      >F  R  T  Q  R  Q  G  L  L  A  R  R  L  P  P  A  P  E  L  T  V  I  L  S  E  A  V  L  R  R  P

82594 GGTGCCGGGGCCGATCGGTGATGGCCGACCAGTCCGGCACCTGCTGGCCGTCGGCGAACGGCACAACATCACCGTACGGGTGCTGCCGCTGG
      >V  P  G  R  S  V  M  A  D  Q  L  R  H  L  L  A  V  G  E  R  H  N  O  T  V  R  V  L  P  L

82686 CCGCCGGCCCGCCCCTGGCCGCCGGAGGCCGGCACGTTCGTGCTGCTGCTCGACTTCCCGCTCTCGGCCCTCGGCTCTCCGACCGAGCCGCCGACC
      >A  A  G  P  P  L  A  A  E  A  G  T  F  V  L  L  D  F  P  L  S  A  L  G  S  P  T  E  P  P  T

82778 GTCTACGTCGAGGGGCTCACGGGCGCGCTCTACCTCGACCAGCCGACCGAGATCGCCGCGGTCTGGAGGGGTCTGGATTCGCT
      >V  Y  V  E  G  L  T  G  A  L  Y  L  D  Q  P  T  E  I  A  A  Y  E  R  V  W  R  G  L  D  S  L

82870 CGCCCTCGGCGCGCGGCAGTCAGCGGAGCTGATCGATGCCATCCGGGGGGAGAGTGCTATGAGTGATCTGACCGGGCCGCTGGCGCACCAG
      >A  L  G  A  R  Q  S  A  E  L  I  D  A  I  R  G  E  C  Y  E  .

82961 CACCCCGAGCGGCACCAACGGGGGACTGGCTCGGAGGTGCGTCGAGGTCATCGTCGGCGTCCGGGACAGCAGCAAGGACCCGGGCG

83053 GGCCGGCCCTGACCGTCCGCGTCGTGCCGCCTTCGTCGTCGAGGTCAAGGCCAACCGGCTCACCGAGGTCTCGCAACGGAA

83145 CCAACCCCCGGCTACGCGGCCTCAGCGCCGCCCCGCGCCTGCTCCCACGCGTCCCCGCGCCTCAGACGTGCCTGCGCCTCAGAC

83237 AGCCCCGGGCCGGGGCCGCAGGGGCGTGCGCCTCCAGACGGCCGCCTTGCCGAGGGCGGCCGACCGCCTTGCCCAGGGGCGGT
                                              <   .  A  R  K  G  L  A  A  D  V  A  K  G  L  A  T

83328 GACGACCAGGGCCACCGAGGGCGGACCACCGAGTCGTCCAGGTGCTGACGGTGCCGGAGAAGCCGGCCCGCGATCTCCTCAGCCGAC
                                              <V  L  A  V  S  P  R  V  V  S  D  D  L  S  V  T  G  S  F  G  A  G  G  A  I  E  E  L  R  R

83420 GCCGGGCGTCGACGGCGCGTCGGCGGTCCATCCGGAGCGCCGGCTCCAGAGGTGGCCACCGGCTGCCAGGGCCGCCGTCGCCTCG
                                              <R  A  D  V  A  A  D  G  T  L  G  L  A  P  E  M  R  L  V  A  V  L  T  A  L  A  A  T  A  E

83512 TCGGGGATCTGCCCGCGGCCAGCGCGCTCGGCCAGCGCCGCCGCGCGTCCTCGTCCGCGGTGGCGTCGCGGTAGCGGTGCACGTG
                                              <D  P  I  Q  G  G  A  L  A  E  A  L  R  R  S  D  R  R  V  T  A  D  T  P  Y  R  H  V  H

83604 GATGAAGCCCAGCTCGGTCTCCTCGACGTCGCGCCACACGCCCGGGCGACCAGGTCGCCGAGGATCGGCGGCCAGCC
                                              <I  F  G  L  E  T  E  E  V  D  R  V  V  G  R  A  V  L  D  G  L  I  R  D  R  L  G  H  R  L  R
```

FIG.11A(72).

83696 GCTGCACCCAGGAGGACGGGGTGTGCGGCGTGTCGGGCGTGTCCAGGACCTCGTCCAGGATCGGTTCGCCGGTGGGCGCGGGGTCC
      < Q V W S S P T H P T D A A M R G L V E D L I P E G T P A P D

83788 GTGACCACCAGGTTCCCATGCATGCGACGTACGCGACCCGGCGGCGGAGGGCCAGTCAGGAGGGGCCATCCGAGGTCGAGGCTGAT
      < T V V L N G D V Y A V R G A L A L E I L V A A M G L D L S I

83880 CCGCGGGCATGGTCGCCTTGCCGTCGTGTCGTCGTACGCGAGGAGCAGCAATTCCTGGCCAGGACACCAGTCATGGCCGGAGACGG
      < R P M

83970 TAGGCGCCTGAGCGCACCCGTGCGCCCCCAACTCGCCCACGAGCGCACTCGCCGGTGAGAGGGGAACCCGCTATACGCAGGCGTTAACA

84062 GGGGGCCCTTCCTTGCGATCAGAAGCGGGGCATACCGCGGCGAACTGGCGGTCGCCGGCACGATGAACATCCGGTCG
      < . F R P M G G F Q R D G A D G L G P V I F M R D

84153 TTGAGGCTCTCGTCGATCGGCGGGTGACGAGGCGCAGGCGCGACTGCTCCAGCGGGCGATGCGCGGGCGAGCACGCA
      < N L S E D I A A T V L R L P L G S Q E L R A I G V P A A L V C

84245 GAGCACGGGTGATGTCGGTGCAGCCCCGCTCGGCCAGGGCCGGCAGCAGTGCTCGCAGGAGCCGCCGGTGGGTCGAGGACCA
      < L V T I D T C G R E A L L R C C H E L S G G T A L M P D L V L

84337 GCACGGGCAGGCCGGCGAGGTCGGCGGCAGCGACTCCATGTACGCGCGGCTCGTCCTCGTCGGGGCGAGGCCGACGAAGCCC
      < V P L G A L D R P L S E M Y A R P E Y T E E D R A L G V F G

84429 ATGGACGACTCGGGGGAGCAGGGCGAGGCGCGGGCGTCGGCCATGCGCCGAGAACCGGGCCCGCGAGACCACGGGGTTGGCCAGCCG
      < M S S E P L L A L A A D A M G L G A R L V P V L L P P N A L R

84521 GGTGCCCTCGGGTCGGTCGGTGACGGGGGTCTGCACCGGGTACTTCTCGACGGGGAAGGAGCGGGCGGCCTGTACAGCAGCATGGTGGTGAGCT
      < T G E A D T V P T Q V P Y K E V P F S R A A E Y V L M T T L E

84613 CGTGCAGCGCGACAGCGACGTCGGCCCCGGAAGTTGGAGAGCGTGCGCGCGTCCCGGCGTCGGTCAGCCGGCGAGCGGCGATGGTCAATGACGTGT
      < H L A A R F N S S D T R A S R M

84705 ACGTCCACGATCGCCCAACCTACCGGAACGCCCGGGCCCCCGAGACACGAGGAGCACGACGCCGCTCACCCGGCCAACCCTGGACGGT

84797 TGGCGGTTCGAAGGTAGGGCAGGTGCCCAAGGTCGGGCCGGCAGTCGGGGTGCGGTGCGGCGTTGCGGGTGCGTAGACTTCCGGG

84889 CATGACGGCGACAGCGACGTCGGCCGTCGGACCTTCTCCGAGTGGGACGATCGGAGACGCGCTTTGCGGAACTTCCTGCACGGCCTGCCG
      > M T A T A T S A R S D L S E L G R S E T A L R N F L H G L P

FIG.11A(73)

84980 GGCGTGGACCAGGTCGGCGGCGGAGCAGCGGGCGGCCCAGCTCGGCACCCGCTCGATCAAGACCACGGCCAAGGCCCGGGCGATCGACCTGGC
> G V D Q V G A E Q R A A Q L G T R S I K T T A K A R A I S L A

85072 GATCCGGATGGTCGACCTGACCACCCTGGAGGGGGCCGACACCCCCGGCAAGGTGCGGGCGCTCGCGGCCAAAGCACTGCGCCCCGACCCGG
> I R M V D L T T L E G A D T P G K V R A L A A K A L R P D P

85164 CCGACCCGTCCTGCCCGCACGTCGGCGCAGTCTGCGTCTACCGGCGATGGTCCGTCACCGGGCGGAGGTGCTGCGCGGATCGGCGGGGTCC
> A D P S C P H V G A V C V Y P A M V P Y V A E V L R G S A G S

85256 GGGGGCGGCCGTCCGGCGGGACCGGACGGCAACGCGCCCGGACCCGGCGTGGTGCACCTGGCCAGCGTGGCCACCGCGTTCCGTCCGGGCA
> G R P S G G P D G N A P A G P G V V H L A S V A T A F P S G Q

85348 GGCACCCCCTGGAGGTCAAGCTCGCCGACACCCGGGCCGCCGTGGCGGCGTGGCCGCAGTGGCCGGCGACGATCGACGAGATCGACATGGTGATCAACCGGGGCGCGTTCC
> A P L E V K L A D T R A A V A A G A D E I D M V I N R G A F

85440 TGGCCGGCCGCTACCGCGAGGTCTACGACGAGATCGTGGCCACCAAACAGCCGTGCGGGACGCCCACCTCAAGGTGATCCTGGAAACCGGC
> L A G R Y R E V Y D E I V A T K Q A C G D A H L K V I L E T G

85532 GAGCTGGCCACGTACGACAACGTGCGCCGCGCGTCCTGGCCATGCTGGCCGGCGGCGACTTCATCAAGACCTCGACGGGCAAGGTTCC
> E L A T Y D N V R R A S W L A M L A G G D F I K T S T G K V P

85624 CGTCGCGGGCGACCCTCCGGTGATGCTGGAGGCGGTCCGCGACTTCCGCGCCAGCGGCGGCGTGGAGGCCGG
> V A A T L P V T L V M L E A V R D F R A A T G R Q V G V K P

85716 CCGGGCGGCATCAAGAACACCAAGGACGCGATCAAGTACCTGGTTATGGTCAACGAGACCGTCGGCCGGACCCGGACTGGTTC
> A G G I K N T K D A I K Y L V M V N E T V G P D W L D P D W F

85808 CGGTTCGGCGCGTCCAGCCTGCTCAACGACCTGCTCATGCAGCGCACCAAGCTGACGACCGGCGTCTACTCCGGTCCCGACTACTTCACCCT
> R F G A S S L L N D L L M Q R T K L T T G V Y S G P D Y F T L

85900 GGACTGAGCGTGATCTTCGAATACGCCCCGCCCGAGTCCCGCTCGGTGGTGGACCTCAAGCCCTCGTACGGGCTGTTCGTCGACGG
> D • > V I F E Y A P A P E S R S V V D L K P S Y G L F V D G

85989 GGAGTTCGTCGACCCGGCCGACGGCGGCGGCTTCAAGTCGGTCAACCCGGCCTCCGAGGAGGTGCTCGCCGAGATCGCCGAGGCGGGCAGCG
> E F V D P A D G G G F K S V N P A S E E V L A E I A E A G S

FIG.11A(74)

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86081  CCGACGTGGACCGGGCGGTCCGCGCCGGACGGGCTACGAGAAGGTGTGGGGCCCGATGCCGGGCCGGGACCGGGCCAAGTACCTGTTC
       >A  D  V  D  R  A  V  R  A  A  R  T  A  Y  E  K  V  W  G  P  M  P  G  R  D  R  A  K  Y  L  F

86173  CGGATCGCCCGGATCATCCAGGAGCGCTCCCGAGAGCGGTGCCGTGCTCCTGGAGTCCCTGGACAACGGCAAACCGATCCGGGAGAGTCGGGACGT
       >R  I  A  R  I  I  Q  E  R  S  R  E  L  A  V  L  E  S  L  D  N  G  K  P  I  R  E  S  R  D  V

86265  CGACCTGCCGCTGGTCGCGCCACTTCTTCTACTACGGGGCTGGGCAGACAAGCTGCCGTACGCGGGCTTCGGCCCCGAACCCCGGCCGC
       >D  L  P  L  V  A  A  H  F  F  Y  Y  A  G  W  A  D  K  L  P  Y  A  G  F  G  P  N  P  R  P

86357  TCGGCGTGGCCGCGCAGGTCATCCGTGGAACTTCCCGCTGCTCATGCTGCTGGAAGATCGCCCCGGCGCTGGCCGCGGCAACACGGTG
       >L  G  V  A  A  Q  V  I  P  Q  N  F  P  L  L  M  L  A  Q  K  I  A  P  A  L  A  A  G  N  T  V

86449  GTGCTCAAGCCGGCGGAGACCACCCCGCTGACCGCGCTGTTCGCGGAGATCTGCCAGCAGGCCGAGCTGCCGGGCGTGGTCAACAT
       >V  L  K  P  A  E  T  T  P  L  T  A  L  L  F  A  E  I  C  Q  Q  A  E  L  P  A  G  V  V  N  I

86541  CGTCACCGGCGCGGGCGACACCGGCCGGGGGCTGGTCGAGCACCCGGGCGTGGACAAGGTCGCCGAGGTCGGCAAGG
       >V  T  G  A  G  D  T  G  R  A  L  V  E  H  P  G  V  D  K  V  A  F  T  G  S  T  E  V  G  K

86633  CCATCGCCCGGTCCGTCGCGGGGACCGGCAAGAAGGTCACCCTGGAGCTGGGCGGCAAGGCGAACATCGTCTTCGACGACGCCCGGTC
       >A  I  A  R  S  V  A  G  T  G  K  K  V  T  L  E  L  G  G  K  A  A  N  I  V  F  D  D  A  P  V

86725  GACCAGGCGGTCGAGGGGATCGTCAACGGCATCTTCTTCAACCAGGGGCACGTCTGCTGCGCCGGGTCGGAGCTGCTCGTGCAGTCGGT
       >D  Q  A  V  E  G  I  V  N  G  I  F  F  N  Q  G  H  V  C  C  A  G  S  E  L  L  V  Q  W  S  V

86817  CGCCGAGCAGGTGCTGGAGTCGCTGAAGCGCCGGATGGCGCTGCTGCGGCTGCGGGTCGGCGACCCGTTGGACAAGAACACCGACATCGGGGCGATCA
       >A  E  Q  V  L  E  S  L  K  R  R  M  A  L  L  R  V  G  D  P  L  D  K  N  T  D  I  G  A  I

86909  ACTCGGCCGCGCAGTTGGCCCGGATCCGCGAGCTGTCCGCCGCGGGGGAGGCGGAGGCAGAGCGGTGGTCGCCGCCGTGCGAGCTGCCC
       >N  S  A  A  Q  L  A  R  I  R  E  L  S  A  A  G  E  A  E  G  A  E  R  W  S  P  P  C  E  L  P

87001  GAGGCGGGGTTCTGGTTCGCGCCGACGATCTTCACGGGGGTCGAGGAGATCATCTTCGGTCCGGTGCTGTC
       >E  R  G  F  W  F  A  P  T  I  F  T  G  V  T  Q  A  H  R  I  A  R  E  E  I  F  G  P  V  L  S

87093  CGTGCTGACCTTCCGCACCCCGGCCGAGGCCGTCGAGAAGGCCAACAACACGCCGTACGGGGGTCTGTCGGCGATCTGGACCGACAAGGGGCT
       >V  L  T  F  R  T  P  A  E  A  V  E  K  A  N  N  T  P  Y  G  L  S  A  G  I  W  T  D  K  G
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FIG.11A(75)

87185 CCCGGATCCTCTGTGGATGGCCGACCGGCTGCGCGCCGACGGCTGGTGTGGGCCAACAAGTTCGACCCGACCTCGCCGTTCGGCGGG

>S R I L W M A D R L R A G V V W A N T F N K F D P T S P F G G

87277 TACAAGGAGTCGGGCTACGGTCGCGAGGGCGGCCGGCACGGGCTCGAGGGGTACCTCGGTGTCTGAGCGGTACGCAAGACGTAC

>Y K E S G Y G R E G G R H G L E G Y L G V .

87368 AAGCTCTTCATCGGCGGGAAGTTCCCGCGACGAGTCGGGACGGTCGTATCTCGTGCAATCGGCAACGGTGTCGTGCTGGCCTCCGCAAG

>V Q S A N V S L A S R K

87458 GACGCGCGGGACGCCGTGGTCGCGCCGCCGCGTGGTCGAAGGGCTGGGCCGGGGCGACGGCGTACAACGGGGTCAGATCCTCTACCGGGT

>D A R D A V V A A R A A V K G W A G A T A Y N R G Q I L Y R V

87550 CGCCGGAGATGCTGGAGGGGCGCCGCGAGCAGTTCGTCGCCTCGGGTCGTGCGGTGTGCGACGAGGTCGACGAGGTCGACGCTGGGTCTGGT

>A E M L E G R R E Q F V A L G V P A D E V D A A I D R W V W

87642 ACGCGGGCTGGTCCGACAAGCTCCCCCAGGTGTACGGGTGCGAACCCGTGTCGCCGGGCGTACTTCAACCTGTCCGCCGAGCCGACG

>Y A G W S D K L P Q V Y G G A N P V A G P Y F N L S A P E P T

87734 GGGGTGGTGGCCGTGGTGCGCCCGCGAGGCCCCGCGCTCGGCCTGGTCAGCGTGATCGCCCCGGCGATCGTCAACACGGTGGT

>G V V A V V A P E A P A L L G L V S V I A P A I V T G N T V V

87826 GGTGGCCGGCCTCGCCGACCCAGCCCCTGGCCTGGTCGACGTGCTGGCCGAGGTGCTGGCCACCTCCGACCTGCCCGGCGGGGTGGTCAACGTCC

>V A A S P T Q P L A S V T L A E V L A T S D L P G G V V N V

87918 TGACCGGTGCGATCACCGAGACGGTGCCGACGCTCGCCGCACGCTGGCCGCACCTGGACGTCAACGCGATCGACCTGACCGGGTGGGCGACGGTCGCTC

>L T G A I T E T V P T L A A H L D V N A I D L T G V G F A S L

88010 GCCACCGAGCTGGAGGTCAGGGCGCGGGAGAACCTCAAGCGGGTGATTCGGCCCGCGCCGGCCGACCACGACTGGTACGCGGACCCCGGGCCT

>A T E L E V R A A E N L K R V I R P A P A D H D W Y A D P G L

88102 CACCCGGATGACGACGCTGCTGGAGACGAAGACGGTCTGGCACCCCAAGGGCGTCTGAGCCACCGACCCGCCCGCCAC

>T R M T T L L E T K T V W H P K G V .

88193 CCGGCCGCCGGAGGCCAGGGGGTGGGGCGCGGGGTGGGGTGGGATCTACTACGAGAGGGGTAGGATTGCCGCCGTGACTCGGTTGGGTGATCTTGAGC

FIG.11A(76)

88284 GGGCGGGTGATGGACGTGCTGTGGGACACCGTCCCGGGCACGTCGGACGGGGTGCGCGAGGTCGCCGAGGCCCTCGACGGCCGCGA
>M D V L W D T V P G T S D G V T V R E V A E A L D G R E

88375 GCTGGGCGTACGACGACGGTGATGACGGTGCTGGACCGGTCTCGCCGGCAAGGGCATGGTGCGGCGCCAGCGGGAGGGGCCTGGCGCTACC
>L A Y T T V M T V L D R L A G K G M V R R Q R E G R A Q R Y

88467 AGGCCGCGGCCAGCCGCGAGGCGCACATCGCCCAGCTCATGCTCGACGCGCTGGACCTCGGCGGCAGCCGGGACGCCGCTGGTGCGCTTC
>Q A A S R E A H I A Q L M L D A L D L G G S R D A A L V R F

88559 GCCCGGTCGGTGACCGGCACCGAGGCCGAGGTGCTGCGCGCCGGCCCTCGGCGCCGCCGAGGCGGGCCCGCTGACCGACCGGGTCGACGCGCC
>A R S V T G T E A E V L R A A L G A E A G G P L T D R V D A P

88651 GCGCGGCCGACCGGGCCGGGCCAGCCGGCCCTGGCCGACGAGGCGACGGACCGGTAGGGCCGTCATGGCGTAGGCCGTGCACTTCGCCG
>R A D R A G Q P A L A D E A T D R . >M A Y A V H F A

88741 CGACGGTCCTGGCCTGCTACCTGACCGCTCAGGTCCTGGCGGTCCACCTGGACGTGGCGGCCCCCGGATCGCGATCGTCTGCTGGCAG
>A T V L A C Y L T A Q V L A A S T W T R A P R I A I V C W Q

88833 GCGGGTCGGGCTCGCGCTCTCCGCGATGGGCCTGCCGATGGCGCTCGGCGGTGGCCGGTGGCGGTTGCT
>A V G L A L G L S A M G L P M A L G V A A Y D R P T G S A L L

88925 CGCCCTGGCCACCGACCTGACCCACGGCACCCTGCCGGCCGGGCTCGGCGCTGTCGGGGTCGGGGTTCGGCATCGGGGG
>A L A T D L T H G T L P A G L G A V H L G L V G G F G I G

89017 CGGGCGCTGCTGCCACGACGGTACGCAGCGGTGCAGGCGGACGTCCGGGGCCAGCGGCAGCACCGGGACCTGCTGCCCCTGGCCCGGCGG
>A L L A T T V R S V Q A T V R A Q R Q H R D L L A L V A R R

89109 GACCCGGAGGTGCCGGGGCGTGGTGCCGGTCGTGCTGGACCATCGAGCGGCGGTACTGCTCGAGCGCGGCGTGCCCGGTGGTGGTCAGCGC
>D P E V P G A L V L D H P S A A A Y C L P G V R P R V V V S A

89201 CGGGGGCGCTCAGCATGCTCGACCGGGCCGAGCTGGCGGCGGTGCTGACCCACGAGCGGGCGCACGAGCGGCCACGACCTTGTCTGC
>G A L S M L D R A E L A A V L T H E R A H A Q E R H D L V L

89293 TGCCGTTCACCGCGCTGTGCCGCGTGCCCTGGTTCCGTTGGGTACGCGACGCGCACGAGCGGGTCGCCCTGCTGGTCGAGATGCGCGCC
>L P F T A L C R A L P W F R W V R D A H E R V A L L V E M R A

FIG. 11A(77)

89385 GACGACAAGGCCCGGGAGCTGCACGCCGAGGCTCCCCTCGCGGGGGGGCCGGTTGCGCGGCCGGCCACCGGATCGGCCGGCCGG
> D D K A R E L H A E A P L A G A L R R G A A A G H R I A P A G

89477 CACCCTCGGCCTGGGCGACCGGGACCTGGACGTCCGGGTGCAGCGGCTCCTGGTCGCGTGCTCGGTGGCCCCGCGGCGCCGCGC
> T L G L G D R D L D V R V Q R L L V A D R P P R L I G A A A

89569 TGGCGGTGGCGGTCACCCTGGTCGCGCTGCCGGTCTCCCTCTTCCTGAGCTGACGCCCGACCGGACGTCCGGACACGCGCGGAC
> L A V A V T L V A L P V S L F L S .

89660 CGGACACGCGTCCGACCGGAGACGGCCTGCGCCCGAGTTGGGCGGGGCCGGTCGCTGCTGCCGTTGCGCGGGCCACCGACATGCGGG
> M D Q L L L A R

89752 GCGATAGGTAGAGAGCCTACGTGTAGTCTTCCTACGAAGGGAGCCTACTACCGGAGGGGCGGCCATGGATCAACTGCTCCTCGCCCGTC
> M D Q L L L A R

89842 TCCAGTTCGCCACGACCACCTGCTCACCTGCACTTCCTCTTCGTCGTGGTCACGCTCGGTCGTCGTCCAGACGGCCTGG
> L Q F A T T S L H F L F V V V T L G L V T L L V G L Q T A W

89934 ACGATCACCGGCAATCCGTCCACGAGCGGCTCAGCTCTACGTGATCAACTACGTGCTCGGCATCGCCACCGGCCT
> T I T G N P V H E R L T R F W G Q L T V I N T V L G I A T G L

90026 GCTCATGGAGTTCCAGTTCGGGCTGAACTGGAGCGGCCTGTCGCGCTACGTCGGCAACGTCTTCGGCGCCCGCGTTGGCGATCGAGACCCTGG
> L M E F Q F G L N W S G L S R Y V G N V F G A P L A I R T L

90118 TCGCGTTCTTCCTGGAGTCCACGTTCCTGGGCATGTGGCATCGGCTGCGTTCGGCATGGTGGCGGAGGTGCGCGAGGTGCGCGACGGGGGT
> V A F F L E S T F L G M W I F G W H R L R R G V H L A L L W G

90210 GTGGCGCTGACGCGCTACGCCGGTTCTGGGCGTTCTGGGTCATGGTGGCGAACGCCGGTCGGCTTCGGCCTTCGGGCTGCGTACGAGGTGCGCGACGGGGT
> V A L T A Y A S A F W V M V A N A W L Q N P V G Y E V R D G V

90302 GGCCCACCTGACGACTTCGGGCGGCGTTGCTGACCAATCCCACCTTCGGGCTTCGGGCGCCTGCGTGGTCGCCGCCGCTGTTCCGGATCGGCCTGGTC
> A H L T D F G A L L T N P T F G L A F G H V V A A A L L T G

90394 GGATGCTGATGGCGGCGGTCTCGGCCTGGCACCTGATCCGGCGCACGGACCCCGGACGCGCTGTTCCGCCACGCGCTGTTCCGCCCAGTTCGGGCGGATCGGGCCTGGTC
> G M L M A A V S A W H L I R R T P D H A L F R T S L R I G L V

90486 ACCGCGGCGGGTCTGGTGCAGGGCTTCGGCTTCGCGCAGTTCGGGCAGACGCAGCCCACCAAGTTCGGCGGCGGCGG
> T A A V S I S L V Q G F G F A Q F G P V G Q T Q P T K F G G G

FIG.11A(78)

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90578 CGGCCAGGCGGCGACGCCCTGGTCGCCGAATGGACCTCCCGGTTCGGGGCCGGGCCGGGCGACTACACCCCGGTTGCTGGCCGACGTCGGGCTCGGTT
      > A  Q  R  D  A  L  V  A  E  W  T  S  R  F  G  P  G  D  Y  T  P  P  V  L  A  D  V  G  L  G

90670 TCATGATCCTGATCGGCCTCCTCGGGCTGTGTCTGTGGCTGCTCCCCCTGCTCTGGCGGGACTGGTTCATCGGCTGCGCTTCCCGCTC
     >F  M  I  L  I  L  L  G  L  C  L  W  L  L  L  P  L  L  W  R  D  W  F  I  R  L  R  F  P  L

90762 TGGCTGATCCTGTGGGCGTGCCCCTTCGTCGCGGTCATCCTCGGGTGGATCGCCCGTGAGGTGGGGCGCCAGCCGTGGGTCGCGTA
      > W  L  I  L  A  L  P  L  P  F  V  A  V  I  L  G  W  I  A  R  E  V  G  R  Q  P  W  V  A  Y

90854 CGGGCTGCTTTCCACCGAGCGGGCGGTCTCGCCGGGGTGCCGCGGGTGATGCTGGCTTCACCGGCGCCCAGCGCGCGGAC
      > G  L  L  S  T  E  R  A  V  S  P  V  A  P  G  V  M  L  A  S  L  I  G  F  T  L  L  L  G  G

90946 TCGCCGGTCGCCAACTGGGTCGTGTTCGCCCGGTACGCCGCGCGGGGAGCCGATCCGCCCTAGGCCCGGCCCCAGCCGCCGAC
     >L  A  V  A  N  W  V  L  F  A  R  Y  A  A  R  G  A  A  D  P  A  L  G  R  R  P  G  P  A  A  D

91038 GAGTCCCGTCCCGTCCCGGCTCCTCGGCTACGGGGAACTGCCTGTGAACTGCCTGGTACGCCCTGGGCTCTTCCTGCCGGTACC
      > V  E  L  A  W  Y  A  L  L  G  L  F  L  A  G  Y  .
     > E  S  R  P  V  P  L  G  .

91127 TGGTCCTCGGCGGCTACGACTACGGCGTCGGCGTCCTGCTGCTCGCCCGGGGCGGCCCTCACCGGCGGTGGGC
     >L  V  L  G  G  Y  D  Y  G  V  G  V  G  L  L  L  A  R  G  G  P  P  A  R  R  A  A  L  T  A  V  G

91219 CCGTTCTTCCTCGGCAACGAGGTCTGGCTGGTGGCGACCGTCGGCATTCTGTTCGGCGCGTTCCCCACCCTGGAGGGGGAACTGCTGTCCGG
     >P  F  F  L  G  N  E  V  W  L  V  A  T  V  G  I  L  F  G  A  F  P  T  L  E  G  E  L  L  S  G

91311 CTTCTACCCCGTCGTCGCCGCGGCCGCGCTGGCCGGGGTGATCATGGTGACCGTCGGCGTTGGGGGCGGGCCGCGACGAGCCGACCC
      > F  Y  P  V  V  A  A  A  L  A  G  V  I  M  V  T  V  G  V  Q  L  R  S  R  P  T  D  E  P  T

91403 GCGCGCGTGGGACCGGATGGTGGCCGCGGGGAGCCTGCTGGCCGCGTTCGGCTGGGGGGCGCTGCTGGCCGGGCTGCTCCAGGGCGTACCG
     >R  A  W  D  R  M  V  A  A  G  S  L  L  A  A  F  G  W  G  A  L  L  A  G  L  L  Q  G  V  P

91495 CTGGCCGCGGACGGGCACGTCACCGGCGTCGGCCACGTGGCCACGCCCTTCGGCGCTGGGCTGGCGATGACGGCCCTGGTGGCGGT
     >L  A  A  D  G  H  V  T  G  V  G  H  V  A  T  P  F  A  A  L  A  G  L  A  M  T  A  L  V  A  V

91587 GCACGGTGCCGACGTTCCTCACGCTGCGTCTGTCCGGCGCTGCGGCGGCCCCGCTGGCGCGCACCGCTCGGTGGCGCTCG
      > H  G  A  T  F  L  T  L  R  L  S  A  A  D  A  A  P  L  A  R  T  A  R  R  L  V  A  V  A  L
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FIG.11A(79)

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91679 CCGCCGTCGCCCTGGCCGCCGTCGCCGGGGCGCGTCTCCGATCGGTACGGCCGCGGACGCAGCGCCCGCTGCCGGCCGTACTGCTGCCGTTG
      >A  A  V  A  L  A  A  V  A  G  A  L  S  D  R  V  R  A  A  R  Q  R  P  L  P  A  V  L  L  P  L

91771 GTACTGGTGGCGGCGCTGCTGGTGGCCCGGCGCGCACGCGCGGGGTGGCCTTCGGCGGCCGCTGGCCGCT
      >V  L  V  A  A  L  L  V  A  R  A  A  H  A  R  H  L  P  G  V  A  F  A  A  T  S  A  A  L  A  L

91863 GCCGGTGGCGGGAGTCGGCGGCGGCGTTGTGGCCCTACGCGCTGGTCTCCACCGTGCCACCGGCATCACTGAGCGTGACGCGGCGG
      >P  V  A  G  V  G  A  A  L  W  P  Y  A  L  V  S  T  V  A  P  T  A  S  L  S  V  T  D  A  A

91955 CCAGCGGGCCGACGCTGACGGTGCTGGGCTGGCTGGCCCTGCCGCTGCCGCTCCTGCCGGCGCTGCTTCCAGGCGATGTGCTGGTGGGTGTTC
      >A  S  G  P  T  L  T  V  L  G  W  L  A  L  P  L  L  P  A  L  L  G  F  Q  A  M  C  W  W  V  F

92047 CGGGGACGAACCGACGCAGGGCACCGGTGCGGTGCTACTGGTGGTGTACTGGTTCGCCGCCCACGTGCTGCTCAGCCTGGGGGGCTGGGGGTGTTC
      >R  G  R  T  D  G  R  A  P  V  Y  W  ·

92138 CGACCTCGCCGTGCTGCTCGGCGGGGTGCTCGGCGCTGCTGACGGCGCTGTCTGGTCGTGGGGGCAGGCCAGCGCCACCGTGCTGGCCGCCGCG
                          >V  L  A  V  L  G  G  L  T  A  L  L  V  V  G  Q  A  T  A  L  A  T  V  L  A  A  A

92229 CTCGACGGGCGGTTGGCCGGGCGCTCGCCGGTTTCCTGGCCGCCGTGGTCGGGCGGGCCCAGGGCCACGGTGGC
      >L  D  G  R  L  A  R  P  A  L  A  G  F  L  A  A  V  V  G  R  A  L  V  A  W  A  Q  G  T  V  A

92321 GGGCGCGGGCGCGCCAAGGCGGCGTCAAGGCGGCCCTGCTGGCGGCCGTCGGGCGTCATGGGCCGGGCTGGGGTCCCGGGTCGCGGGCAGC
      >A  R  A  A  A  T  V  K  A  A  L  R  A  D  L  L  A  A  V  G  R  H  G  P  G  W  V  A  G  Q

92413 GGGCCGGGCCAGCTCGCCACCCTGGCCGGGCGGGGCCTGGACGCCCTGGACGCCTACTTCACGGGCTACCTTCCGCAGCTCGTGCTCAGCGTC
      >R  A  G  Q  L  A  T  L  A  G  R  G  L  D  A  L  D  A  Y  F  T  G  Y  L  P  Q  L  V  L  S  V

92505 ACCGTCCCGGTGGCCGTGCTGGCCCGGATCACCTTCGCCGGGCTCGGCGTCATCGTGCTGCCGTGATCCCGGTCTT
      >T  V  P  V  A  V  L  A  R  I  T  F  A  D  W  G  S  A  V  I  V  A  L  T  L  P  L  I  P  V  F

92597 CGGGGCGCTGCTCGGCTGGCAGGCGCAGGCCGCCACCGAGCGGCAGTGGCGGCGGCTGTCGACGCTCGGCGGCCACTTCCTCGACATGGTCG
      >G  A  L  L  G  W  Q  A  Q  A  A  T  E  R  Q  W  R  R  L  S  T  L  G  G  H  F  L  D  M  V

92689 CCGGGCCTGCCACGCTGCGCGCGTTCGGCCGCGCCCGGGGCCAGGGTGGTCGCGAGGTCGTGGTGCGGCGGATGGCCGGGGCCGCGACGATG
      >A  G  L  P  R  L  R  A  F  G  R  A  R  G  Q  V  E  V  V  R  R  M  A  D  G  H  R  A  A  T  M
```

FIG.11A(80)

92781 CGCACGGCTGCGCGGATCGCGTTCCTGTCCGCGCTGGTGCTGGAGCTGGTCGCCACCCTGTCGGTGCTGCGCGGTGTGCGCGGTGGGCATCCG
> R T L R I A F L S A L V L E L V A T L S V A L V A V P V G I R

92873 GCTGCTCGGCGGCGGGCTGGCGCTGTCCACCGCGCTGCTGGTGCTGCTGCTCACCCCGGAGGCGTACCTGCCGCTGCGGGCGGCGGCAGCC
> L L G G G L A L S T A L L V L L L T P E A Y L P L R A A G S

92965 GGTTCCACGCGCCAGCATGAGGGGCTGGCGGCGCTGGACGAGGCACTGACCCTCTCGCGCCGACCCGACGGCGGCCACCGGCGGGGTCG
> R F H A S M E G L A A L D E A L T L S A A D P T A T A G S

93057 CGGCCGTCCCGACGGCGCGCCGAGATCCGGTCGAGGGCGTCGGTCGAGAGCGGACCGGCGCTGCGCTACGGACGTCACGCTGAC
> R P V P D G R A E I P F E G V T V A Y E R T V A L R D V T L T

93149 AATCCGGCCCGGCGAGCGGGATCGTCGGGCCGAGCGGCGGGGGCCAAGAGCACCCTGCTCAACCTGCTGTCGGCTTCGTGCCCGA
> I R P G E R I A I V G P S G A G K S T L L N L L G F V A P

93241 CGGCAGGGCCGGGTCACCGTGGGGTCGGTCGACCTGGCCGGTGCCGACCCGGACGGCGGCGTGCCGGTGCCGCAACGGGCC
> T Q G R V T V G G V D L A G A D P D G W R R Q V A W V P Q R A

93333 CACCTCTTCGCCGCCTGCCTGACGAACATCCGGTCTCGGTGCCCCGACGGCGCTCGCCGGCGGTCGCCGCCGCGCCGC
> H L F A A S L T D N I R L G A P G T P D A A L A G A V A A A A

93425 GCTGGACGAGGTGGTCGCCCTGCCCGACGGGCTCGACACCGTGCTCGGTGAGCGGCACGGCCTGTCCAGCGGACGGCGGCAGCGGG
> L D E V V A A L P D G L D T V L G E R G H G L S S G Q R Q R

93517 TCGCCCTGGCCCGGGCCGTTCCTGCGGGACGCGCCCGTGTTGCTGCTGGACGAGCCGACACCGCGCTGGAGGCCGAGGGGGGTG
> V A L A R A F L R D A P V V L L D E P T A R L D T A S E A G V

93609 CTGGCCGCGACCCGCCACCGCTCGTCGCGGGCGAACCGCCCTGTTGGTGGCCCACCGGCCGGCTCTCCGACGCGGATCCTGCG
> L A A T R R L V A G R T A L L V A H R P A L L S D A D R I L R

93701 GGTCGAGGAAGGCCGGGTCACCGAGCTGACCACCACCCCGGCCACAGGGGTGACCCCGGGGGTGCCGGAGCGGCTGCCGGAGGCGGGGC
> V E E G R V T E L T T T P A T G V T P G P G E A A A G P A G

FIG.11A(81)

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93793  AGGTGCCCCCGCCCCGGCCCGGAGAGGGGGGCCCGATGAGCACCGGTCCGCCATCCCGTGCCGGCCGACGGG
       >Q  V  A  P  A  P  A  G  E  G  G  A  A  R  .
                                       >M  S  T  G  P  A  D  D  A  F  A  I  P  L  Q  A  D  G

93884  GCCCCGGTGGCCGGCGGGGGCAGCGTCCGGGCGGCCGAGGCGCGCCGTGCTCGGCGCCGGCCGTACCTGGGCCGGCTGGTCGGCGGGGTCT
       >A  P  V  A  G  G  S  V  R  A  A  E  R  A  V  L  R  L  A  R  P  Y  L  G  R  L  V  G  A  G  L

93976  GCTCGCCGCCGCCACCGAGTTCGCCGGCCTGGCCCTGATGGCCACCTGGCTGCTGATGAGCGCCGCCGGCAGGCCTCGCCGGCCACGATGCCGTG
       >L  A  A  T  E  F  A  G  L  A  L  M  A  T  W  L  L  M  S  A  A  G  R  P  P  L  D

94068  GGCTCACCGTGGCGGATCGTGTGCGGGTCCGGGCGATCAGCGGCGTGTTCCGCTACACCGAGCGGCTCGCCGGCCACGATGCCGTG
       >R  L  T  V  A  I  V  A  V  R  A  L  A  I  S  R  G  V  F  R  Y  T  E  R  L  A  G  H  D  A  V

94160  CTGCGGATGATCACCGACGTCCGGGCCGGGGTCTTCGCCGCGCTGGCCGCCAGGCGCGACGCCGCGCGGCAGCGCACCGGCGACGCGCTGAG
       >L  R  M  I  T  D  V  R  A  G  V  F  A  A  L  A  A  R  R  D  A  A  R  Q  R  T  G  D  A  L  S

94252  CCGGGCTCGTGTCCGACGTGGAGGCCGTGCAGGACCTGCTGCTGCTCCGGGTGCTGGTCCCGGGCGCCGCGGCCACCGGTGGTGCTGGCCG
       >R  L  V  S  D  V  E  A  V  Q  D  L  L  L  R  V  L  V  P  G  A  A  A  T  V  V  S  V  L  A

94344  TGGCCCGGGGCCACCACCATCTCGCTCCCCGCCGCCGGGGTGCTGGCGCTGGGCCTGCTCGTCGCCGGCGTGGCCCTGCCGCTGGCCGCCACC
       >V  A  G  A  T  T  I  S  L  P  A  A  G  V  L  A  L  G  L  L  V  A  G  V  A  L  P  L  A  A  T

94436  GCGCTGACCCGCCACGCCGACCGGGTAGCGCCGCTGCGGGGCGCCCTGGCCCGCGATGCGGTGGACCTGGTGCACGGCGCCGACCT
       >A  L  T  R  H  A  A  D  R  V  A  P  L  R  G  A  L  A  R  D  A  V  D  L  V  H  G  A  A  D  L

94528  GGCCGCGTTCGGTGCCACCGGGTACGCGCTGGACGCCGCGGCCGATCGGGCGCGCCGCGGAACGACGGCTCGCGCCGCACCG
       >A  A  F  G  A  T  G  Y  A  L  D  A  A  A  D  R  A  R  R  L  A  R  L  E  R  R  L  A  A  T

94620  GCTTCGCCGTGGACGCGGGCGGGGCGCTCGTGGTCGCCGGTGGTGGTCACCGCGGTGGTCACCGCGGTCGGGGGGTG
       >G  F  A  V  D  A  A  G  A  L  V  A  G  V  T  A  G  T  V  V  V  T  A  L  R  D  G  V  G  G  V

94712  CTGGTCGGGGTGCTGGCCGTTCCCTGGCCGTCGCTGGCCGTCGAGGTGGCCGGGCGCCCAGGCGCACCCAGCTCCGGGC
       >L  V  G  V  L  A  V  G  S  L  A  A  V  E  V  A  L  A  L  V  G  A  A  R  Q  R  T  R  L  F  A

94804  CGGGCTGGTCCGGGTGGCCGCCCTGCTGACCGCCCCGCAGGCCGACGCCCCGGCCGCCACCCCGCCGGGTGCCGCGCGCGCCGTCG
       >G  L  V  R  V  A  A  L  L  T  A  P  Q  A  D  A  P  A  A  T  P  P  G  A  A  R  A  A  A  V
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FIG.11A(82)

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94896 GTGCGGGCCCGCCACGACGTGCGCTTCGACGCGGTGGCCGTGACGGTTCACCGTGGTACCGGGCACCGCCCGGCCCTGGACCGGGTCACCCTGGACCTG
      >G  A  G  P  H  D  V  R  G  D  A  V  T  V  R  Y  R  A  G  T  A  P  A  L  D  R  V  T  L  D  L

94988 CCGGCCGGCCGCCGGGTCGCCGTGGTCGGGCCGTCGGGCGCGGGCAAGAGCACCCTCGCCGTCCTCACCGGGACCGTGCGACCGAGCA
      >P  A  G  R  R  V  A  V  G  P  S  G  A  G  K  S  T  L  A  A  V  L  T  G  T  V  R  P  E  Q

95080 GGGCCGGGTCACCCTCGACGGCGCCGACCTGTCGGCGTACCCGGTCGAGGAACTGCCCCGGGCCGTCGGCGGCCTCGCCGAGGCGTACG
      >G  R  V  T  L  D  G  A  D  L  S  A  Y  P  V  E  E  L  P  R  A  V  G  G  L  L  A  E  A  Y

95172 TCTTCCACGCCACCGGTCCGGGAGAACTGCTGTCGGCCGGCAGAACCTGCTGCTCGGGCCGGCCGCCGACGAGGCGGAGCTGACCGCCGCGACGCGGGCGGCCGGCCTG
      >V  F  H  A  T  V  R  E  N  L  L  L  G  R  P  A  A  D  E  A  E  L  T  A  A  T  R  A  A  G  L

95264 CTGGACTGGGTGCACGCCCCAGCCGGGTGGGACACCGTGGTCGGCGAGGGCGGACAGCTCTCCGGGCCAGCGGCAGCGGCCTCGC
      >L  D  W  V  H  A  Q  P  A  G  W  D  T  V  V  G  E  E  G  G  Q  L  S  G  G  Q  R  Q  R  L  A

95356 GCTGGCCCGGGGCGCTGGCGCTGGCGGCGCCCGCGGGCGTGCTCGGGCCCGGGTGCTCGGTGGTGCTCGACGAGCCGACCGAGGGTGCTCG
      >L  A  R  A  L  L  A  A  P  G  V  L  V  L  D  E  P  T  E  G  L  D  P  S  A  A  D  A  V  L

95448 CCTCGGGCGCTGGCGGCGGCGCCCCGCGCGGGCCACTCGGTGCTGCTGATCAGCCACCGGCTCAGCGGCCTCGCCGACCTCGACGAGATCGTGGTG
      >A  S  A  L  A  A  T  P  A  G  H  S  V  L  L  I  S  H  R  L  S  G  L  A  D  L  D  E  I  V  V

95540 CTCGACGCGCGGCCGGGTGGTCCAGGAGGTGCAGCGCCACGAGTTGGTCGCCGCGCCGGGACCAGTGGCTGCTCCAGGAGGC
      >L  D  A  G  R  V  V  Q  E  G  R  H  D  E  L  V  A  A  P  G  W  Y  R  D  Q  W  L  L  Q  E  A

95632 GGCCGAGCGGGGGTACCTGGCCCTGACCCCGCGCCCGTGAGCGCGGCTCGGCAGTCGGCCAGTCACCGCATGGCAGGCT
      >A  E  R  G  Y  L  A  L  T  P  R  P  .

95723 CGTCGGCATGGTGCGCTGCGACGACGTACTCGTGAAGGAGCGGCTGCGCGAGTTGAGCGACCGGCTGCACGGGCTCAAGGCCG
                        >M  V  R  C  D  D  V  L  V  K  E  R  L  R  E  L  S  D  R  L  H  G  P  A  R  L  K  A

95814 ACCTGCTGGCCGAGCGGCACGCGCTGCAGGACGCGGTTGCAGGACGCCGTCGAGGCGTACCGGGACGGCGGCCTGCCGGCGGCGGAGGCGCGGGCA
      >D  L  L  A  E  A  R  H  A  L  Q  D  A  V  E  A  Y  R  D  G  G  L  P  A  A  E  E  R  R  A

95906 GTGGCCGAGTTCGGCGAGCCCGCGCGCCTCGCCCCGGCGTACCAGGCGGGAGCTGGCGGCCGGGTCGCTGCGCGGGCTGTCCCTGCGGGTGCT
      >V  A  E  F  G  E  P  A  R  L  A  P  A  Y  Q  A  E  L  A  A  G  S  L  R  G  L  S  L  R  V  L
```

FIG.11A(83)

95998 CGCGGTCGCCGGGGTCCTGGTCGTCGCGGGGATCTGACCTGGCAGGGGTCGAGCTGGAGCGGCGGCCCCGGCCCGGCGGCCTACCGCC
> A V A G V L V V A G D L T W Q G S S W S G G P G P P A A Y R

96090 TGCTGTCCGCCTCGGTCGACGGCATCTGGCTGGGCGCGGTTGTGCTGTCGGTCGTCGCGGTCGCCCGGTTGCCCGGTGGGCG
>L L S A S V D G I W L G A V V L S V A G L L L V A A S A R W A

96182 CACCCGGCCCTGCCCCGGCTCGCCGGCTGGCTGGGGTCTCGGGCTGACCGCCACGCTCGTCCTGGGCGTGGCGCCGGCCCTGTACGC
> H P A L P R L A R L T G L G L T A T L V L G V A T G A A L Y A

96274 CTGGTCGATCGGGCTCTGGGAGGCGGCCCGGACCTGGCCACCTGGCCGATGCTCGTGGGCGCGCTGGTCTGCGGGGGTTCTTCTGGATCGGGTC
> W S I G L W E A A R T W P P M L V G A L V C G A G F F W I G

marker   junction

96366 GGGCGGCCCGGTCCTGGCTGCTCTCGGCACGCGCCGACCGGCCGGCGTAGTCGGGTGGGCGGCGGCGTCAGGCCGCGGTCGGCGG
>R A A R S W L L S A R R P A G P A .   < · A P T A P

96457 GGGTGGTCGCCGGAGGAACTGCGCGGTCGCGCTGAACTCCCGGCCGCTGAGGGCCCGGCGGAGGGCCCGGCCGGAGTCGGTCGGTCAGC
< T D G L F Q G V T A S F E R W G A R E G A L A R R G S D T L

96549 TCGTAGGTGCGGGCGTCGCGGCGTTGACGGTGCTCCAACTGCTGACCGTGCCAGCGCGGGTAGATCGT
<E Y T R R E R G N V T S W S S V V H G A R E L R R L A P Y I T

96641 CCCGGTAGGCAGATCGAGGCTGCCCTCGCTGCGCGCCCTGGCCGATGATGGCCTGAGCCGTGCAGCCGCCGTTCCAGCCACCGGCGA
< G T P L D L S G E S R A R L A E I I A Y G H L A G R E L V A L

96733 GCAGCAGCGCGTCGAGGTGTCCGCCAGCGCGGCCTTCATAGGTAGTAGCAAGACTACTTGTGGGCCACTGCGCGCGCCACCGGGGGTGCGG
< L L A D L H G H L A Q A K M

96824 GCACCGGGCCTCCTAAGCCGCCCACTAGGGTATGTGCCCCAGAGTCACTCGGCGGCCGGGTGGGCAGCCGGAAGCACAC
> V G S P K H T

96914 GGAGGTCAGGGTGGCCGCCAGTCGCCCCAACGGCCGGCCACGGCCGACGAGCTGAGCTCGACGAGGAGGACGACGAGCCGCCGCAGAGGGTCGAAG
> E V S V A R Q S P Q R P D A D E P E L D E T D G T A A E V E

FIG.11A(84)

97006 AGGACGGGCGGCGCCCGTCGGGCGGCCAGGAGGACGCCGACCGCGCGCTGTGGGACGAGCTGCGCATCGACCCGGTCGAGATCGCCCTGCCCGCCGGC
> E D G A R P S A Q D A D R A L W D E L R I D P V E I A L P A G

97098 ACCGGCTACACGCTGCGGGCGTACCGCGGCACGGGAGTTGACCCCGACGCGCGCGAGCGGCGACCAGGAGCGTGCTCCTGGCCCG
> T G Y T L R A Y R P A R E L T P T D V A E R D Q D D P F L A R

97190 CCGGCAGGCGGTCGAGACGGCGGAGACGGAGGACGAGGTCATCATCCTCGACGAGGAGGTGGCCGCGAGTTCGCCGAGGCGGACGCGGAGG
> R Q A V E T D E D E D E V I I L D E E V A A E F A E A D A E

97282 AGGCCGGCGGGGAAGTCCCGCTCCGCGAAGCCCGCGCCGGGACTGCCGAGCGCCGGGAGCGCCACAGACGCGGAGGAGGAG
>E A G G K S R S R K P R A D A D S D D A G A A T D A D A E E E

97374 CCGGACTCCGACGAGGAGGGGCGGCGAGAGGTTCCGGTTCTTCCTCAGCCACCGGGGCAGGCTGCTGTTCAAGACGCCGAATC
> P D S D E D E A G D E E V P V F L S H R G R L L L F K T P E S

97466 CCTCGTCAGCTTCGTCCGGTCCGGCGCACCCAACGACATGTCTCAACTGGACAGCTGGAATGAACTGTCCGAACGGGTGGAGCCGGCCGACA
> L V S F V R S G A P N D M S Q L D S W N E L S E R V E P A D

97558 TCGTCCCGCTCGACGAGGACACCTACGAGCTGGACCTGGTCGTGGAGAACCTGCGGGGTGGGCACGACACCTGGGACTCGGCGCTGCTGATC
>I V P L D E D T Y E L D L V V E N L R G G H D T W D S A L L I

97650 GAGCCGGGCGAGGTGGCCCGGGAGCGTGCCGGCGTATGCCCTGCGTCTGCCCGCGTGTTGGACACATGCTCTCCGCGGCCTCCAGCCTGCGACGACCTG
> E P A R W P G T S R M P C V C P P C W T C S P P A S T T W

97742 GACGAGGCGGCTGCGCGACCGCCACGGCCAACGGGCGGCTTCCTGCGCGGGGGCTGGGGGCTGAGGAAAATCGGCGGCTGAGACGGCGGAGTC
> T R R C A P R P T A G S G A S S A A G G .

97833 TCGGTTGGGCACCATTGTCGGCAAGATCTCTGCGGGTCGTGCAAGATCTCTGCGGGTCGTGGACTGGCGCGACTGACACGTTCCAGGGAGCATCAGTCTCTGGCAGAGAAAG

                                        BamHI
                                  junction marker

97925 ACCAGTCCCGGGAGGAGGACGACGCTGTGTGGCGCTCGTCGTGCGCGTCTGGCCTCGGCGATCCGGCCGACCGGCCTCGGCC
98017 GGTTCGGCGCTGACGTCGCTGTGGTCGACGACGCAGGTCGGCGACGATCGGCGACGACCGGCTACGCTGCTCAGCT
98109 GGTCGTGCTACTCGTGGAGCGGTCGGGGCCGAGCGGGCTGCGATCGGCGGCCGAGCAGCGACGACCACACGGTCACCTCGCTGCTGAGTG

FIG.11A(85)

98201 CCGCCGGGGGTCCACTGGCGATCGCCGGGACGACGACTCGGTGGACGACGACTTGCCGAGCGGTTCGCCGACGACGACTGCTGGAGGAGATGCA
> M Q

98292 GTCCGCGCCGGCCGAGCGGCGGGTCGGGGCTGGCCCGGGCGCTCGGCCCGGGCGCTCTCGGCGGTCTCCAGGCCGGCGCTGGCCCGGGCGCTCTCCAGCCGGCC
> S A P A E R R A V G L A R A L Q A G A L S A V T L P A P R D

98384 TCGGCGGCTACAAGCAGGTCCTCTCGGCGCACGCGGCGCTCGCCAGCGGCCGGCACTCCGCGCCGTGGCGCTGCGGCAGGTGCTGCGGGAG
> L A G Y K Q V L S A H A A L A S G R H S A A V A L R E V L R E

98476 CTCTACCCGGCCGCGCTGCGCGTACCCGGATCCGGAACCCGGAGCCGGTGCCCTGGCGCTGGTGTTGGACGCCCTGCCGGAGCCCGGGATGCTGGG
> L Y P A A L R A Y P D P A E P V A L A V L D A L P E P G M L G

98568 CGGGACGATCGCCCGGGGCCGGGAGGTGTCGGTGGCCGCGGACGCCATCGCCGCGCACCTCGCCGCGGGGTGGCCGACGAAGGCAAGA
> G T I A R G R E V S V A A D A I A A H L A A D G V A D E G K

98660 TCAACGATGCGGTGACCGCGCTGCGGGTCGCCATCGCCGAGACCCCGCGCCGGGCGCTCACCTCCGCCGTGGCGGAG
> I N D A V T A L R V A I A E T P R R A A V S R A L T S A V A E

98752 ACGGTCCGTCAGGCGGTGGCCTCGGTGCGCGCCTGTGACGCGGGCTGCGAGGCCCTGGTCGGCGCTGGGCGGTCACCCCAG
> T V R Q A V A S V R A C D A G C E A L V G A L D A R V T T P T

98844 CCCGGTGCCGGGGCGGCGGCCGCGCGCGGGCGAGCCGGTCGCCGAGCTGCCCGGCGCACTGCGCGCACTGCGGGCCACAGAGC
> P V P G R R A A A R G E P V A E L P G A G L R A L R P T E

98936 CCGGAGCCGGTCCCCGGCCGCCGGAGCCCGTCCCGAGCCGGTCCCCGGCGGGTCCCTGCCCGCCCAGCCCCGCCCGCTGGGCCCGCCGCCGGTC
> P E P V P G R R S R P E P V P G G S L P A Q P R P L G P P P V

99028 GCGCCCGGAGCCGGTCGCTCCGCCGGTCGCCCCGCGACCCCGACCCGGCTCCCGGCCACCCCGCCGGTCTCCGGCCCGCCGTCGCC
> A P E P V A P P P V A P R P I T P A A S A T P P V S G P P S P

99120 CGAGCCGCGGCGGCTGATCGACAACCCGGCCAACCGGCGGCCGGTCTCCGCGCCGCCACCGGGGATCACCCGATCGCGCCGAGCC
> E P R R L I D N P A N R R P V S A P P P P P P G I T P I A P S

99212 AGCGCGAGCGCGGGGGTCGTGCCGCCGGCCGAGGCCGGTGAGCCGTTCCGGCCCACGCTGACCACCGCGCGCGATCCAGAACGCGCGGGGCGGGAG
> Q R E R G S V P P A E A G E P F R P T L T T A A I Q N A R A E

FIG.11A(86)

99304 CGGCAGGCACCATCATCCGCCTCTGCCCCAAGACGACGGGGGAGTCCGCGCCGCCGCCCACCGGGGCTTCAGCGCCACCGACCTGAGCGT
>R Q R T I I P P R P K T T G E S A P P P T G G F S A T D L S V

99396 CCCGGTGCCGACCCCGCGTCCCGGCCAGGAGTCCGCTCCCCCGGCGGGCAACTGGCCGCTGGTCAACAACCCCGAGGACCCCGCA
>P V P T P R P G Q E S A P P G S R A N W P L V N N P E D P A

99488 ACAGCTCCCGAACAATCCGTCGCGCGGCGCCCTTGGAGGATCGGGCGAAGCGGCAGATCGACGCGCCAGGTGGTCCGCGCCGGCC
>D S S P N N P V A R R P L E D R A K R Q I D A P T Q V V P P A

99580 GAGGGCCGGGGTCACCCCGGCTCGCCGACGACCTGCCCCAGGAGCCACCGATGCTGCGGCTGGTCGAGCCGCCGCTGGCCGACCG
>E G R V T P P W L A D D L P Q R P P M L R L V E P P L A D R

99672 GGCACTGGGGGATGGGCCGGGCCAGGCTGCCGCCGACCCGCGCCTGGAGCCCCCGCTGCGCCTGGTCGACCGCGGCGAGGCCGCGCCG
>A L R D G P G Q A A D P R L E P P L R L V D R G E A A R A

99764 GCCGTCCCGCGCGCCGGAGCCCGCGCCGAGCGGGCCCCGCGGAACACCGGTCCCGGTCCGGTCAGCGGGTCCCGTTGGAGGAGCGGGCCCGAC
>G R P A P E P R P E R A P A E H R S P L G Q R V P L E E R P D

99856 ATGGAACATCGGACGGCGCCCCCGCAGCCGTCGCGCCGATGGAGCGGCGTACCCCGCGATCTCCGACGAGGGGGACGGGCGACCT
>M E H R T A P P Q P S R S A P M E R R T P P I S D E G D G D L

99948 GCTGATCTTCGCCGCGCCAAGTCGGCCTGGTTCGTCGGGCACGGGGATCCGAGATGGACTGGTCGAGCACGTGCCGACACCGGGTGGC
>L I F A A K S A W F V G H G D E S E M D W S S T A S T G W

100040 AGGCCGGCCGAGCAGCCGCCGCCCGGCGGTGGGCGCCGATACCAAGGCCGGGTTGCCCAAGCGTGCCGCAGGCCAACCTGGTTCCGGGC
>Q A A E Q A A R P A V G A D T K A G L P K R V P Q A N L V P G

100132 TCCCCCCTGCGCGAGGAGCGTCCCCTACGGATAGTCCGCGACGCCGCCAGCCTCGCCGAGAACACGGCGTACTTCGGGGCTGGCGTCG
>S P L R E E R P L R I V R D A A S L A E N T T G Y F R G W R R

100224 CGGGCAGGAGAGATCGGCGGGTTCGCCGTCGGCGGCCGGCCGGGCCGGGAGGCAGCCGGCGGGGACTTCACCCGGGACACCGGCGACCGAG
>G Q E I G G F A V G G R P G R E A A G G W D F T R D T G D R

100316 ACGACGACCGGGGAGTACGAGTACCGGTCGGCCGGCTACCGGTCGCCGGCTACCGGTGGGACCGGTGGGCGGCCACCGAAGAGCAACCCTGGCCGGCCGCCTGACGTC
>D D D R E Y E Y R S A G Y R S .

100407 CCGTGCTGGCGTACGGGCGTAGCAACCCGACCGACCGGTGGGACCGACACCGAAGAGCAACCCTGGCCGGCCGCCTGACGTC

FIG.11A(87)

100499 CCGCAGGGACGGTGACGGCTACTGGCCGTCCCCCGGGAAGGTTGCGAGGCGGTCGGGGGCGCACAGGCGGCTGTCAGGGCCGCTCCTGAGCCG
100591 CCCTACGGAATGGGCTAGCCCTACGGAATCGAGCGCCGGCCGCCCGGTGGCGTCGAGTTCGCCTCCAGCCGGTCCCCAAACAGCCGGGAC
100683 GCGCCCGACGCGGCCCGGCGCGGTGCCGGTCCGGCGCGTCCGTCGTCGATCAGGCCGGCGCCGGCGAGCGGCGCATCGTGAGCA
                     < . A P A V A R S R R M T L V

100774 CGTACTGACGACCAGCGAGATCAGCACGTGCTTCGTCGACTCCCGGTTCCGGGGCGTCGCAGGCCACCACGGTCGTGCGAGATCGCGAGC
                     < Y E V L S I L V H K T S E R N R A D C A V V P V D H S I A L

100866 GCGTCCGGAGCGTCCTGCGGGGTCGTGGTCATCCGTCGTACTGCCGTCGAAGCAGTTGATGGCCAGCAGCCGCCGATGCTCGAAGAAGTC
                     <A D R V D Q P D H Y Q M G D F C N I A V L Y P L R R H E F F D

100958 GATGGCCGCGAAGCAGTCGGCCGACAGTGCCGCCGGGTGTCGACCAGGACCACCGCGTCGTCCCACATGAACCAGA
                     <I A A F C D A L R R T D V L V V A G I A G R C L E D W M F W F

101050 ACCGGGTCTGGCCCGGGGTGCCGAACAGGTACAGGATCAGGTCCCGGTCGAGATACGGCCGAGTCCATCGCCACCGTGGTCGTCGTC
                     < R T Q G P T G F L Y L I L D R D I S I R G F D M A V T T T

101142 TCGCCCGGCACCTGCGCGGGTGTCGTCGAGCGCCCAGCGCGGGAGGTCATGATCGCCTCGGTGGTCAGCGGCGTGATCTCCGAGACCGAGCC
                     <E G P V Q R T D D V G V G A S T M I A E T T L P T I E S V S G

101234 GACCAGCGCGTCGTCTTGCCGACGCCGAACCCACCGGGATAACGATCTTCGCCGACGTCACCGCGCTCGGGACCAGGCGGGGTGCGACA
                     <V L T T K G V G F G G A I V K A S T V R G S P V P P R H S M

101326 TGTCAGAGCCTGCGAAGTCCACTCAGCCACCCTCTCCAGCCAGTTCAGTGCCACCGCTCGTCGGAGTCGTCGCCAGGATGGTCGGCTCGTGGA
                     <<. L R R L G S L V R E L L E T G V A D D S D D L I T P E H V

101417 CTGCGACCAGGCCGTCGTCGCCATGTCGGCCGATGAGCACCCTAGCCACCGCGCCGAGCTGCATCCGCGCGATCTCGGCAAGCGAC
                     < A V L G D T A M D A I L V R A V G L P L Q M R A A I E A L S

101509 TGCACGCGTCCGTCGCACAGCGCGGGCGGCGATGTACTGGTCGTCTGGCCCTGGCCAGCGCCCGACCGCCGCACCGTCGT
                     <Q V R G D C L A A I Y Q H E R G Q G G N S S A A A R G R V T T

101601 CTCGACGAGCGCGCCTCCAACGCGTCCAGCGAGTGTCCAGCGCGAGGGGTACGACGCGGGGGTACGACGACCAACGCGCCAGTGCGGCTCGT
                     <E V L A E L A I D L R P R T R G R T V A Y P R V L A G T P E D

FIG.11A(88)

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101693 CACGATCCATGTCGCCGGCTCACCTCCTTCGTCCCCGACACGGCTGAACCCGTGGAACCCGTGGTTCTTGCCACCCCGCCCGAC
       < R  D  M  D  G  S  V  E  K  T  G  S  V

101784 CCATCGGCCAGCCGCGGTGGGTCAGCCCATCATCCCACAGTGTCTGCGGGGTCAACGCGTCGCCACCCGGTCGCGACCAGGAGGGC
       < ·  G  M  M  G  V  T  T  R  P  Q  P  T  L  A  D  G  V  R  D  V  L  L  A

101875 CATCTCGTATCCGACCTGCCGCGAGTCGCGACACGGCTACGGCGGCGGCAGCAGGACGGCGAAGGACGAGCGAGCCGTCGAGATGGACATCAGGAACAGGAAGC
       < M  E  Y  G  V  Q  G  V  D  C  S  R  A  A  L  V  A  F  S  S  G  D  S  I  S  M  L  F  L  F  G

101967 CGTTGTCCATCTGACCAGGTCTGCAGCACCGGCACCGCCCTCGAAGCAGCAGCGGTGCGGTGCCGACACC
       < N  D  M  E  V  V  T  Q  L  V  A  G  G  E  F  C  R  A  A  G  Q  T  L  S  V  L  G  S  A  I

102059 GCGGGCGAGCTGGTCGGCCCCGTCACGCGGCTCGTGACGACGAGGTCTCGTGACGACGCGGAGCAGAGACCGTCCGGGAGACGGCGTGCGCGACACC
       < A  A  L  Q  D  A  R  D  R  P  L  D  R  S  S  A  L  L  G  D  A  S  V  A  V  A  H  A  V  G

102151 GGGCACCCGGTCGGCGAAGTTGGCCAGCAGCCAACCGAGATCCTGCGTAGTTGTCATCCTGTTGCTCATCCTCCTTGCTCCGGCCACCG
       < P  V  ·  ·         G  Q  Q  E  K  Q  G  S  G  A  V  P

102242 GGCCTGAGCCAGCCAGAGACTGCAGCTGCGCGGGATTGCTGCCCACCCGGAGCTGCCTCCGGGTTGGTCGGGTTGCTGCGTCGGGTACGCCACGCTGCACG
       < G  S  G  S  Q  S  S  Q  Q  G  G  P  A  A  E  P  N  T  P  N  G  D  P  E  T  R  G  R  Q  V

102334 CCTCGATGGTATGCCGAGAGCGCGGGACGCCCTCCGGGACGCGCTGGACGTGGGCTTCTCCACCCGCCAGGCACGAG
       < G  R  H  Y  A  S  L  L  G  R  V  G  E  P  T  R  Q  V  S  T  T  P  K  E  V  G  G  P  V  L

102426 TTGGGCCATCGGCACCCGCTTCGGCAGGCCCTTGCGGGTGGTCTCCCGGCACCGGAGCGGGACCTCGGTGGCCGCGCCGAGGCGGCCGCCAGCCGTCGT
       < Q  A  M  P  V  R  K  P  L  G  K  R  T  T  E  A  V  P  V  E  T  A  A  S  A  A  R  W  S  P  P

102518 CCCGCGGCAGTCTGCTGCCAGGGCGTGGGCCGCGTGGGCGTGGGCGGTGCCACCGTTGTTGTTCGGC
       < A  A  T  Q  W  A  H  A  Q  P  T  P  R  R  G  A  F  G  E  A  P  G  P  R  T  G  G  N  T  P

102610 GACCCGTTGTCGCGGCGACGTCGCGGGGAGCTGTTCCTGCGGCCATCGGGGTGTCTGCCATCGGGGTGTGTCTGTTACCTGGTCGTTCGCGGCGGCCGGCCG
       < S  G  N  D  R  P  M  G  G  A  M  P  R  D  A  M  P  A  N  G  T  T  G  P  A  P  T  Q  V  V  P  R

102702 GCCGGTGACGTCGACGCGGGAGAACTGTTGGGTGGGCTCCCGGCGCGTTCGCCGGCGCATTGGTCGCGGCGCGACGCGCGGCCG
       < G  T  V  D  V  A  S  F  Q  Q  T  V  A  A  N  A  P  S  G  A  G  N  T  A  R  Q  A  V  G  A  T
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FIG.11A(89)

102794 TCTCCTCCGAACCCGAGGGCGGGTACGGAAGCCAGGCCGACTCGAGCTCCCGGAAGATCGGCAGCTCCATCGTCTCGTCCGGTACCGCTGC
       < E E S G S R R T R G W A S E L E R G I P L E M T E D A Y R Q

102886 TGCCGGTTCTGGGCCTGCTGAACGACGGCGCTGACGGGCGTGGGCGGGTTCGTCGGCTGCTCGGCCGGTGCTCGGCCACTCGGTGCTCGG
       < Q R N Q A V P T S R A P T P P T T P Q T A P T S P V E T S P

102978 CACCCGGGGGCAGCTCCGTGGTCATGTCCAGGGCTGCGGCGAGGCGCTCCGGCGCGGGGTGACCGGCTCGGCGCGGCCACCGGCGGCC
       < V R P L E T T M D L A A A L R E P V P P T V P E P A A V P P W

103070 AGGCCGGCGGCGCCACGGGCGCCTGGGCCGCCGACGGGCAGCGGCCGCCGAGTACGGCCGAGTACGGCCGGGCGGTGCCG
       < A P P A V P A Q A D P V P R S P L P Q A S Y P Q G S V P T G

103162 AACGGGCTGACCGGAGACACGGGCGTGCCGAACGGCTGCCGGGTCCGGGGTCGGGSVPAAS...
       < F P Q G S V P T G F P Q G S V P A A S V P Q G S V P F V S V P

103254 CGGTGCGAACACCGGCGCACCGAGACCCGGGCCTCCAGCCTGTGCTCGGGGATGCCGGCTGCT
       < P A S V P P V S V P P P T W G R A E P S S P L Q R P I A P Q Q

103346 GGCCGCTGCTGGCGGATCGGCATCGCAGGCCCGCCGGACCGCCGCGGGCGGCGGCA
       < G S S A P D G D G S A R R Q P L P D S S Q G N S T R G A A A

103438 CCGCCAGCGGTGCCACTGGCCCCGGTCCAGGTCGGAGCACGGGCTGACGCGGGCGTGGCCGTTGGCG
       < G A T G S A G T L D S W A P M S R M S G T S A P T G H G N R

103530 CGAGGCCGGGTCGAACGACCGGCGGCCCCAGGGTTACCTGGTTCGCCCGAGTGCCCGCTGGGTGTCGCCGGGTTGTTGC
       < S A P D G D R G G L T V Q N G S H G P R Q T P A P T A P N N G

103622 CGAAGGCCGGAAGGCCACCCAGGGCCGGGGGAGGGCAGCGGCCCGGGCTGC
       < F A A F A G L A P P A G G P Q S S T L S A P P A P L A G P Q

103714 TGGAACCGGCCGGGCGAGAGCGCCCGGGGCCACCAGCACGGTGGGCAGGGTGACGTCGGGCAGCTC
       < Q F R G S L A R P V L V T T P L T V D A V T G R D T G P R L E

103806 GACCTTGACCCGTGCCGGGACGCGCCAACCGGGACGCCCATCATCCGGGAGACGACCCACGTCCACCTGCGCGGCGGAGGGCGA
       < V K V G H R S A L R A V V V L G M M R R S V A V D V Q P P S A L

FIG.11A(90)

103898 GGCGGTCGTTGAGGTCGTGTAGCTGCTCGGCGCTGATGCCCGGTCCTCGACGTAGAGGTTGGCCCGGTCGCCGACCGGCGGGCC
< R D N L D H L Q E A S I G I G R D E V Y L N A R D G V R R A

103990 TCCACCATCACCTGCGCTCGGGCGGCGAGAAGGCGGTCGCGTTGTTGAACAGCTCGGCGCGTTGTTGACCGGCGTGCGC
<E V M V Q S D P P S F A T A N D G L E A V L H V L D N V A H A

104082 GGGCGACCTCGATGTCACGGTCGATCACCCGAACTCGATCCGGGTGTAGTGCTGACCTCGGACTGGGCGGCCGCAGCACGTCGATCAGTG
<A V E I D R D I V G F E I R T Y H E V E S Q A A R L V D I L A

104174 CCGCCGGCTCGCGCTGCACGCGGGTGGAGTCGGCCCCGGCGAGCACCAGGTTCTCGTTGCGGCCATCCGGGTGGCCAGGTGGTCG
< A P E R Q V R T S D A G A L V L L N E D N R R M R T A L H D

104266 AGCTGGAACAGCTCGGCCAGCCGGTCCGGGTCCTCCTCGCCCGGCTCCTCAGCCGGTCGAGGTGGCCGATCAGCCGGTCGACCAGGATCTGCGA
<L Q F L E A L R D P D E E G R E L R D L H F I L R D V L I Q S

104358 ACGGCGGGCCAGGTTGACGAACATGGTCGCGACGGAGCGGCGCAGGCCTGCTCCGCCGTCCCGCGTCCCAGGTGGACCGCGT
< R R A L N V F M T A V S A R L A A Q E A A T R V A E L H V A N

104450 TGAACGCCTCGTCACCTGGCCAGCTCGTCCTTGCTGCCGACCTCGGCGATCTGTTGCGCCTGCTCGTTGGCGCCTGCACCGGGGGAGAGCTGG
< F A E T V Q G F E D K S R V P L P E A I Q N A A Q V P S L Q

104542 CTGGAAAACTGCGGGATCGCGGCGAGCCGGGGCAACGGCCTGGGGCAAACGTACTGGGCGATGCTGAGCGCACCCTGGCGCAGGTCGCGCAGCGA
<S S G Q P D R L R A V A Q P L G T Q A I S L A G Q R L D R L S

104634 GCGGGCCATCGACCGGGCGACCAGGTACGCGGACAGGATGGCCAGCAGCATGCCGAGCAGCAGCAGGCCGGTCTGGAGGAACACCGTGCGCT
< R A M S R A V L Y A F L I A L L L M G L L G T Q L F V T R Q

104726 GTACGTCGGAGCGGGAGCGGGAGGCGTGGCGCTGCTTCGCCTCGACCACGTTGGCGCTGGCGGATCAGTTGGCGCTACGGATCAGTTGGCGCGGACCATG
< V D S R L A D A Q K V V N G D L K A E V T R I L K A S A V M

104818 GCCGCGGTCCCACTGATCCGGCCCGAACGGCGGTTGGCCAGTGCTGGCCATGCTGGTGTTGCCGTTGCCGTGGCCGCAGCCGGTCGTTCTGCGCCTCGCG
<A A D W Q D P G F P A N A M S G N T N G D L W G T Y N Q A E R

104910 CCGGTCGCGCCGGCGACGGTCTGGTCGTGCAGGTCGAGGTCGGCCACCGCCTTGAAGCTTTGCAGTGCCTGCTGCTGCGCCGG
<R D G G A V T Q D H L D S E D L S A V A K F S Q L A Q Q Q G T

FIG.11A(91)

105002 TGCCGCTGGCGATGTAGTCGGTGCGCAGGATGGGGGTCAACTCGCGCTGGATCAGCGCCCGGTGCACCACGACCCGGCGACCGAGAGGTAT
        < G S A I T D T R L I P T L E R Q I L A R H V V V R R V S L Y

105094 TCCTTCTCCCGGGCGACGGCTGCCGCGGCATCCGGTGTCGTTGTCGTTGGCGAGGTGGGTGGCGGAGTCGCGGATGGACAG
        <E K E R A V A A A R M R D S L D N D G A L H T A S D R I S L

105186 CAGGTCGTTGATGAGCAGCCCTGTACGCCTGCATGGCGTCGATGATCTTCAACTTGCCGTTGAAGACCTGGCTGCGGGGTGCCGGGAGGTCCT
        < L D N I L G E T A Q M A D I I K L K G N F V Q S R T G P L D K

105278 TCAGGTTCTGGTCGATCCGTCGGCAGGCCCTGCTGGCAGGCCGTCGACCTCCCCGCGTGTTGCCAGGTACGGCACCTTGTCC
        < L N Q D I G D L L G E L S S P L G D V E G R Q Q L Y P V K D

105370 TGGTCGACCCGGATGTTGACCCGGTTGTACGCCTTCTGGTACGCTCTGGTCGCGCCTGGCCTTCGCGCCCGAGCAGCAACACCGGCGGAGGT
        <Q D V R I N V R N Y A E Q Y A K A Q D G S A G L L V A S T

105462 GCGTTCGTCCTGGAGGCTGTTGACCAGGTCGCCGACGGTAGCCACCAGGTCGCCGGAGCGGTTGGCGTTGTTCAGCGTTCCA
        < R E D Q L S N V L D G S Y G V L N A L D G S R N A N N L T E L

105554 GGTTGTGTCGACGAGGCCACTGGTCGCCGACGACGCCGTGGCGATGGTCGGCGACGATCATGATGAGACGCTTGGACCAGATCGGCATGTC
        < N D V L G S T G V V V T A I T P V I M I L G L K S E I P M

105645 GCGGAGCCGGCCGACCGGCCGAGCAGTCGCGACAGGAGGAGAACCCGGCTCTTCGGTCGTTGCTCACGTCACCGCCTCGCGATCACAGC
        > H R L V L L A G P S G S G K S T I A Q Q T G L P V L C L D D F

105737 GTTCGCGCGGTGCCCCGGCCAACGCTCGGCGGGTCGACCCGCGGGTCGATTCCATCACGCCGTGTTCCAAAGAGAAAGCCCA
        > Y K D G D D P T L P R Q N G L V D W D S P Q S W D A G A A V

105829 GGCTGGCCGTCGCCGAGGTGTGATGAGATGTTGATGCAATTTGCTCGCAATCCGTCCAGCCGGAGTGACTGACAGTAATGGATCACCCC
        > M D H P

105919 CACCGGCCTCGTCCTGCTCGCCCGGCCCTTCGGGCTCCGGAAAGTCGTACATAGCCCAACAAACCGGGCTTCCTGCTTCTTTGTCTGGACGACTT
        > H R L V L L A G P S G S G K S T I A Q Q T G L P V L C L D D F

106011 CTACAAGGATGGTGATGACCCTACGTTACCGCGCCAAAACGGTCTTGTGGACTGGGACTCACCCAGTCGTGGGACGCCGGCGGCCGTGG.
        > Y K G D D D P T L P R Q N G L V D W D S P Q S W D A G A A V

106103 AAACGATTGCCCGGCGCTGGCGCGCGGGACGGCGCAAGGCCGAAGTGCCGGTTTATGCGATCGGCGCGGGTGGCCACCCGGACATTCGAG
        >E T I A R L A R D G K A E V P P V Y A I G A D R R V A T R T F E

FIG.11A(92)

106195 GTCGCCGGATCGCCACTTTTCGTCGCCGAAGGGATTTTCGGCGCCGAGATCGTCGAGGAATGCCGACGGCGAGGGCTGCTCGCCGGGGGGTA
       > V A G S P L F V A E G I F A A E I V E E C R R R G L L A G A Y

106287 CGCGCTGCGCGGCCGGCGGCACCACCTTTTCCGGCGGCTCCCGGCGCAGCGCAAGGCTCCCGGAATGCTGCTGCGGC
       > A L R R P R G T T F F R R L A R D L A E Q R K A P G M L L R

106379 GCGGCCTGGCCCTGCTGCGCGGAGCCGGCGGTGCTGCGGCGCCAGGGCGGGGTCGGGCTGGGCGCCCGGCCCGCGAGGTGCTGCGC
       > R G L A L L R A E P A V L R R Q A G L G A H P A P A R E V L P

106471 CGGGTGGCCGACCTGCTCGCCGGGCACCCGCACCACCCCTGATCAGCCCAGCAGCTTCCCGTACGCCGGCTTGATCACCTCGTCGATGAT
       > R V A D L L A G H P H H P • G L L K G Y A P K I V E D I I

106561 GGCCAGCCGGCTCGTCGAACGGGATGAACGCTCTTCATCGGCGTTGATGGTGAACCATTGGAGCTCCTTCCAGCCGGTAGCCGAAGGCCTCCG
       > A L R E D F P I F A S K M A N I T F W Q L E K W G Y G F A E A

106653 CCAGCAGGCCATCTCCCGGGACATGCCGCTCATCGAGGTGCCGGTTGTCGGTGTTCACCGTGGTCTCATCAGCCGGTGTGCGCTCATCGCGCAGAAGC
       < L L A M E R S M S T G S M L R N D T N V T V R F R L D R L L

                                                          BamHI
                                                      junction marker

106745 CCGATCGGGTGCTGCGGCGATGCGACGCGCGCCGGTGCTGCGACGCGGTTCGACGACGACGGGCACAGCTTCCAGCGGGATCCGCTTGTCCCGCACGTA
       < G I P H E A I S A A A G T Q V N S S P C L E L P I R K D R V Y

106837 CGCGGGCCAGCCGGCCGGCCCAGCACACGGGCGGGGGTCGCGGGGTGATGTCGTCCACGATGCGGGCCGAGGCGGTCCGCGAGGCGGTCCGCGCCACCACT
       < A A L R G L V P P D G P T I D D V I R V G H G L R D A G C W Q

106929 GGATGGCCTGCCAGATCGACGCGCAGCCGCTCGCCGGCGTGAATGGTGAAGTGGAAGTTCTCCCGTCAGTACTGAAGGCGTCC
       < I A Q W I S P L G F A E G A H I T F H F N E R Q L Y E F A D

107021 AGGTGCCGGGTGGGCGGGGAATCCCGGCCTCCGGGCCCGGGCGATGTCGAAGCCCACCACGCCGTCGGTGCCGCCACCGCCAGTTCGGCGAT
       < L H R T P P F G A E A G A I D F G V V G A D R H R V A L E A I

107113 CTCCTGCGACCGGCGGGCGGTGCCGCCATGGCGGTGAGCCAGGGTGCCGACCGGGGATGGCGGATCGGGATGGCGCGCCCTCGG
       < E Q S R A A H R M A T L L T G V R I P H G A D A A L A A G E A

FIG.11A(93)

107205 CGAACCCGGCGAGGACCGGCTCGACCACCTGTCGACCACCTGTCTGCTCGGGGGCGAACCGCACCTCGGCGTAGACG
< F G A V V A E V V E E D L T L D R E L H Q E P A F R V E A Y V

107297 ACCCCGTCGGCGGCGGCCAGGTCCAGCGCGCACTCCTGGCCACCCGCGCAGTGCGGGGGCGTGTGGGCGAACGT
> V G D A A L D L A C E Q A V R R L A P A T Q M V A V T H A F T

107389 CTCCAGGTAGCGCTCCAGCGAGCCGGAGTTCGCCGCCGCATTGCCGGACGAACCAGCAGCGGCCGAGCTCGTGGCCGA
< E L Y R E L S G S N A A V F W R G L A E P D T T P L E H G V

107481 CCTCGGGGCGGCCAGTCGACGATCGTGCCGGCCGCAGGCCGCGTCGTGCAGCAGCAGCCTTGGGGACTTGACGATGTCCTCG
< E A A L E V I T A P R L G G D L H D H L L A K P V K I D E

107573 TATGAGATTGCGACCATGCCCAGACCCTAGTAGCGACCGGGGTCGCCGACGAGGATGTCCAGGTGATGGACCCC
< Y S I A V M   > M D P

107662 CGCATCGTCGACCGGCTGCCCGGTTGCCCGGTCTGCGCGGAACCGCTCACCGAGGCCCGGCGGCTGCCGCGCCG
> R I V D R L R C P V C A E P L T E A A G T T R A L R C P R R

107754 GCACAGCTTCGACGTTGCCCGCCAGGGGTACGTCGACCTGCTCGCCGGGCGCGCGCCACGCGTGGGCGACACCGCCGAGATGGTGGCCGCCC
> H S F D V A R Q G Y V D L L A G R A P H V G D T A E M V A A

107846 GCGCCGACTTCCTGCGCCGGGCCACTACGACACGCTCTCGGCCGCTGCCGCGCTGAGCCACCGCCGGAGGCC
> R A D F L A A G H Y D T L S A A L A A A A L A A L S H P P E A

107938 CCCGGAGCGGGAGCGGCGTCGGCGGCAAAGACGGGCAGGATGCCCAAGCCGGGCCGTCCGCCGGGCGGACAGCC
> P G A D A S A G K D G Q D A Q G R D A S A G H D A S A G Q P

108030 GGCCGTCGGCGGGCGGGAGCGTACCCGCCGCTGGTGGTGGACGCCGGCGCACCTGCTGGCCGCGCTGCCGACGCCGTGG
> A V G T Y P L V V D A G A G T G R H L A A V L A A L P D A V

108122 GCCTGGCCCTGGACGTCTCCAAGCCGCTGCGCCGGCGCCGCGCCCACCCGCGCCGCTGGCGGCGG
> G L A L D V S K P A L R R A R A H P R A A A A L A D T W R R

108214 CTTCCGCTGGCCGACGCGAGCGTCGCCGTGCTGCTCGACGTCTTCGCGCCGCGGAACGGCGCAGGGCGCGGAGTTCCGCCGGCGCGTGCTGCACCCGGCCGGG
> L P L A D A S V A V L L D V F A P R N G A E F R R V L H P A G

FIG.11A(94)

108306 CGCGCTGCTCGTGGTCACCCCGCCGAGGA CACCTGCCGGAACTGGTCGACCTGCTCGACCTGCTGAAGGTCGACCCCGACAAGGCGGACC
> A L L V V T P A E D H L A E L V D S L D L L K V D P D K A D

108398 GGGTCGCCGGGAGCCTGGCCGGCCACTTCGAGCAGACAGCCGAGAGCGTGCTGCGGGCCCGGGAACTCGAGCTGACCGGCCAGGTGGCCACC
>R V A G S L A G H F E Q T A E S V L R A R L E L T G R Q V A T

108490 CTGGTCGGGATGGGACCCAGCGCCTGGCACACGACCGACCCTGCGCCCGGATCGCCGCGCTACCGGCCGGGTCGGGTGACCCT
> L V G M G P S A W H T D P A T L A A R I A A L P E P V R V T L

108582 CGCGGGTACGGGCTCGGGGTGTACCGGCCGCGGTGACCGGGCGGCGGCCCGCGCTCGACCTCTTCCAGCCCGGGGCTC
> A V R L G V Y R P R •

< • T S L D V E E W G P P E

108674 CTCGTGGTAGGGCCCTGCCAGGACCACCGGCCCACTCCAGGGCGTCGCCGATCGGCGTTGGCGTTGCAGGCGGGGCGGGGGGGGGACC
< E H Y P G R L V V A W E L A W R R Q G I A N A D V L G P P S R

108766 GCCCGTCGCGCTCCAGTCCAGGTACGCCCAGTCGAGGCAGTAGTGCAGGTCGAGCAGGCCGCGCCGGTGCTGGGGCGCGGCC
< G D R E L E L Y A W D L C Y H L D L L A A A D A P H Q P A A

108858 AGGATGCGGAGCGCCACTGCTGGAAGCTCTCCCGCCCGATGTGCCAGGCGCTCGTGCGACCGGCGTCGGGTC
< L I R S R W Q Q F S E G G A I H P L R E V L R E D V P L T P D

108950 GAGCTGCTTGGCCGGCCGAGCACCCAGGCACCGGAGAACAGGCGTCGTGGTGCAGCAGACCGGTGCCCGGCCGCCATCA
< L Q K A L G L V W A L S F L A D H H L V F S R H D G R G G M V

109042 CGAACTGCCACTCCGGGCGGGGTGACCAGGTCGACCAGGTGGGAGTTGAGCAGCCAGTCATGCGCCGCCTGCGCCGGAAACACCGG
< F Q W E P P T V L D V L H S N L L W S M A A Q P M G F C R

109134 GCCAGGATCACGTCGACACGTGACGGCCGATGCGCCTCGATCTCGAGCGGCCTCGGCCCGGCTCCCACACCAGGGGAA
< A L I V H L V A I R A E I E V T P R L E I E D G P E W V

109225 ACTGGCTCGGTGGCAGCGGCAGCCCCAGCCGGGACCAGTCGTCCAGGCTGGCGTCAGGACCTCTCGCGGGTCGGGAGCGGAAAACGCGCACG

109317 GCTCAGATCCCGTGTCAGTCGCATCGGCGGTTCGGGGAGGATAGCGGTTCACGACGAGCGGCACCACGGCGGGG

109409 CGGGGGGCGGGGCCGGTTCAGCGGAGGCTCGGGCGGTCGGGGGGTCGGGGGAGATCCGTACCGCGCCCGGACCGCCTCG

109501 GCCAGCGCCGCCGGGGATCC
       BamHI

FIG.11A(95)

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   1 GTCTTCGGGGAACGCCACGGGAACCTCCTCGCCAGAACCTGACGCGTAACCGGTGGGCACCCGCGGCGGCGATCAACCGGTGCGGTGGTTCCCAGGTTCCGGCCGCCGCGCGGCCCCG

 122 ACGCACCGGCCGCCCCCGGTGTGAGGAAGGGGACCATCTCTAGCGTAGGCGTTAACAAGGGCCCTTCCTT TCA CCG CAG GTG CAG GAC GTC TCC GGC GAG GGT GCG
                                                                          <  •   R   L   H   L   V   D   G   A   L   T   R

 228 CGG GCC CGC CCG GGT GTC GAC GGT GTC CAG CAG CCG GCC CAC CTC CGC GGT CGG GAC GCC ACC GCC GGG CAG CAG CAC
     < P   G   A   R   T   D   V   L   L   R   G   D   A   D   V   G   T   A   V   G   T   V   E   A   G   G   P   L   L   V

 318 CCG CAC CGG TCT GAC GGT GCA GGC CGC GTA CGC GCC GTC CCC GCT GCG GTC GCG CCG GTG GCG CCA GCG
     < R   V   P   R   G   V   T   A   C   A   A   L   Y   A   D   R   L   G   S   A   V   A   D   G   G   A   H   R   W   R

 408 GTC GTA CCA GTC GGC GAC GTC CAG CAG CTC GCG CAG CTC GTC GGC GTC GGC GAG GGT CGA GGT GGC
     < D   Y   W   D   A   V   S   R   L   L   A   R   L   L   P   D   R   D   T   A   V   A   G   A   L   Q   L   S   T   A

 498 CGG CAG GCC GGT CGG GTT CGC GGC GGG CTC GTC GGC GCG CAG GGT GAC GAT GCC GAG GGG CTG GTC CGG
     < P   L   G   T   P   N   A   P   L   E   D   A   R   L   T   V   N   L   G   I   G   L   V   I   A   P   P   Q   D   P

 588 GGC CGG GCC GGG CAC CGC CTC GTT GGG CCA CTT GGC GTC GAT CAG CAG GTC CCA GGC GGC GTC
     < A   P   G   P   V   A   E   A   L   I   G   A   C   K   A   D   G   I   L   L   D   N   P   W   K   L   A   D   L

 678 CTC GGC GCG CAC CGC GCC CGC GTA CCC GGT CGC GGC GGG GCC CGG CGG CCA GAC GTC
     < E   A   L   R   A   V   A   E   V   L   A   V   G   A   L   L   P   L   W   G   Y   G   T   A   P   P   P   W   D

 768 GCG CTC CGC GAC AGC GCC CGG CGG CCG GGC GGG GCC CCG GCG CCG GCC
     < R   E   A   V   A   E   G   P   R   L   L   V   S   T   A   I   G   A   R   P   P   S   Q   W   V   R   G   R   R   G

 858 CCG GCC GGC GGT CTG CCG CTC GGC GAT CAC GAG GCC CTC CGC GGA TCG GCC CGC GTT GGT GGT CGA GCC
     < R   G   A   T   Q   R   E   A   I   V   V   L   G   E   P   E   G   S   R   A   A   E   A   V   D   A   N   T   S   G

 948 GGT CTC GGC GCG TAG CTC CAG GGC GTG CGG GGC GGT CAG CGC CGA CAG CGG GCG ATC
     < T   E   A   R   u   E   L   R   A   W   P   G   H   P   A   T   L   A   R   R   L   R   A   A   S   L   P   P   R   D

1038 CAG GTC GGT GTA CGG CGA GCC GGG CAT CCCGCCAGCGCTACGGCCGCCCGCCCCGGACGCGGCGGGTGCCCGAGCCCGGTTGCCCGAGCCCGGTTGCTCGGATCACAGCACGGGATCAACATCACAGCACGGGATCAACATCAGCACGGCGAAGCTGGCG
     < L   D   T   Y   P   S   G   P   M

1145 CAC ACC GTC GGC CAC CTG AAC CAT CGT TAT ATT CCG TGG GTG ACT ACC GAG ACC GGG ATC AAC ATC CAC AGC ACG GCG GGC AAG CTG GCG
     > V   T   T   E   T   G   I   N   I   H   S   T   A   G   K   L   A
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FIG.12A

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1235 GAC CTG GAG CGA CGG GTC GAC GAG GCG GTG CAC GCC GGG TCC GCG CGG GCG GTG TCC AAG CAG CAC GCG CGG GGC AAG AAG ACG GCG CGG
    >D   L   E   R   R   V   D   E   A   V   H   A   G   S   A   R   A   V   S   K   Q   H   A   R   G   K   K   T   A   R

1325 GAG CGG ATC GGG CTG CTC CTC GAC GAG GGG TCC TTC GTC GAG CTG GAC GGG TTC GCC CGG CAC CGG TCC ACC AAC TTC GGC CTG GAC CGC
    >E   R   I   G   L   L   L   D   E   G   S   F   V   E   L   D   G   F   A   R   H   R   S   T   N   F   G   L   D   R

1415 ACC CGC CCG TAC GGC GAC GGG GTC ATC ACC GGC TAC GGG ACG GTC GAC GGC CGG CAG GTC TGC TTC GCG CAG GAC GAG TTC ACG GTC TTC
    >T   R   P   Y   G   D   G   V   I   T   G   Y   G   T   V   D   G   R   Q   V   C   F   A   Q   D   E   T   V   F

1505 GGC GGC TCC CTC GGC GAG GTG TTC GGC GAA AAG ATC GTC AAG GTC ATG GAC CTC GCC ATG AAG ATC GGC TGC CCG GTC GTC GGC ATC AAC
    >G   G   S   L   G   E   V   F   G   E   K   I   V   K   V   M   D   L   A   M   K   I   G   C   P   V   V   G   I   N

1595 GAC TCC GGC GGC GCC CGC ATC CAG GAG GGC GTG GCG TCC CTC GGG CTC TAC GGC GAG ATC TTC TTC CGC AAC GTC CGC GCC AGC GGC GTC
    >D   S   G   G   A   R   I   Q   E   G   V   A   S   L   G   L   Y   G   E   I   F   F   R   N   V   R   A   S   G   V

1685 ATC CCG CAG ATC TCC CTG ATC ATG GGC CCG TGC GCC GGC GGC GCG GTG TAT TCT CCG GCG GTC ACC GAC TTC ACC GTC ATG GTC GAC CAG
    >I   P   Q   I   S   L   I   M   G   P   C   A   G   G   A   V   Y   S   P   A   V   T   D   F   T   V   M   V   D   Q

1775 ACC TCG CAC ATG TTC ATC ACC GGC CCC GAC GTG ATC AAG ACG GTC ACC GGC GAG GAC GTC GGC ATG GAG GAA CTG GGT GGC GCG CGC ACC
    >T   S   H   M   F   I   T   G   P   D   V   I   K   T   V   T   G   E   D   V   G   M   E   E   L   G   G   A   R   T

1865 CAC AAC GCG CGC AGC GGC AAC GCG CAC TAC CTC GGT ACC GAC GAG GAG GAC GCG ATC GAG TAC GTC AAG GCG CTG CTG TCG TAC CTG CCG
    >H   N   A   R   S   G   N   A   H   Y   L   G   T   D   E   E   D   A   I   E   Y   V   K   A   L   L   S   Y   L   P

1955 TCG AAC AAC CTG GAC GAG CCG CCG GTC TTC GAC GCC CCG GCC GAC GTC GCC ATC AGC GAC GCG GAC CGG GAG CTC GAC AGC CTC GTC CCG
    >S   N   N   L   D   E   P   P   V   F   D   A   P   A   D   V   A   I   S   D   A   D   R   E   L   D   S   L   V   P

2045 GAC TCG GCG AAC CAG CCG TAC GAC ATG CAC CGG GTC ATC GAG CAC GTG CTG GAC GAC GGG GAG TTC CTG GAG GTC CAG CCG CTG TAC GCG
    >D   S   A   N   Q   P   Y   D   M   H   R   V   I   E   H   V   L   D   D   G   E   F   L   E   V   Q   P   L   Y   A

2135 CAG AAC ATG GTG GTC GGC TTC GGT CGA ATC GAG GGA CGA CCG GTC GGC GTC GTG GCC AAC CAG CCG ATG CAC CTC GCC GGC ACG CTG GAC
    >Q   N   M   V   V   G   F   G   R   I   E   G   R   P   V   G   V   V   A   N   Q   P   M   H   L   A   G   T   L   D

2225 ATC GCC GCG TCG GAG AAG GCC GCC CGG TTC GTG CGC ACC TGC GAC GCG TTC AAC ATC CCC GTG CTG ACC TTC GTG GAC GTG CCC GGG TTC
    >I   A   A   S   E   K   A   A   R   F   V   R   T   C   D   A   F   N   I   P   V   L   T   F   V   D   V   P   G   F
```

FIG.12B

```
2315 CTA CCC ACC GGC CAG GAG TGG GAC GGC ATC ATC CGG CGC GCG AAG CTC ATC TAC GCC GAG GCG ACC GTC CCG AAG GTC
    >  L   P   T   G   Q   E   W   D   G   I   I   R   R   A   K   L   I   Y   A   E   A   T   V   P   K   V

2405 ACC GTG ATC ACC CGC AAG GTG TAC GCG GGG TAC GAC GTG ATG GGC TCC AAG CAC CTG GGC GCG GAT CTG AAC TTC GCC TGG CCG ACC
    >  T   V   I   T   R   K   V   Y   A   G   Y   D   V   M   G   S   K   H   L   G   A   D   L   N   F   A   W   P   T

2495 GCG CAG ATC GCG GTG ATG GGC GCG CAG GGC GAC ACC CTG GCC AAC CCG TAC GTG GAG CTG GCC GCC GAG GAC CCG GCC GCC GTG CGC
    >  A   Q   I   A   V   M   G   A   Q   G   D   T   L   A   N   P   Y   V   E   L   A   A   E   D   P   A   A   V   R

2585 GCC GAG AAG ATC GCC GAG TAC GAG GAC ACC CTG GCC AAC CCG TAC GTC GAC TCG GTG ATC CCG CCG CAC
    >  A   E   K   I   A   E   Y   E   D   T   L   A   N   P   Y   V   D   S   V   I   P   P   H

2675 GAG ACG CGT ACC CAG ATC GTC CGG GCG TTG CGG GTG CTG CGC GCC AAG CGC GAG ACG CTC CCG GCC AAG AAG CAC GGC AAC ATC CCG CTC
    >  E   T   R   T   Q   I   V   R   A   L   R   V   L   R   A   K   R   E   T   L   P   A   K   K   H   G   N   I   P   L

2765 TAG GCGCGGGTGCAGGGAGGGCCCCTGTCACGCGATCCGTGCAGCAGGGCCCCCTCCCGACGCGGGCGCCGG TCA GCA CGC CGG GTT
    >  ·                                                                    <   ·   C   A   P   N

2878 GGC GGC GAG GCA CAT CCG CCG GGC CGT GGC GCG GCC CAG TTC GAG CAG CTC CGC GTC GCT GGT CTC CGC GTC CGG GCC GTC GAC
    <  A   A   L   C   M   R   R   A   A   T   R   G   L   E   L   L   E   A   D   S   T   E   R   P   G   D   P   G   D   V

2968 GCC CAA CCC GCG CTC GGG GAC GAT GAC GGT CAC CAG CCG TTC CGG CGG GTA CCC CAC GTC GAG GGG
    <  G   L   G   R   E   P   V   I   V   T   L   D   G   V   R   V   I   M   R   T   E   P   P   Y   G   V   D   L   P

3058 CTT GCC CGT CGT GGG GTC CAC CGG GGA CAT CAC GGT GTG CCG CAA CAC CGC CTC GTC GCG GAA GTC GCG GGC GAT CGT CTG CCA
    <  K   G   T   T   P   D   V   P   S   M   V   T   H   R   L   V   V   A   E   D   G   A   F   D   R   A   I   T   Q   W

3148 GGT GTG GGC CAC CGA GAT CGC GCC GCC GTC ACG GGC CGC AAC GGG CCG GCA GGT CGC CGC GTC
    <  T   H   A   V   S   I   A   G   R   G   D   D   L   P   R   V   A   T   D   S   W   R   A   C   T   T   A   R   D

3238 CAG GTC GGC GAG GAG CCG GGC GGC GTC GGC GCG GCG CCG GAC CAT CGA GGG GAC CGG CCC CGC CTG CTT GCC CAC GGC GCC
    <  L   D   A   L   L   R   G   A   P   A   P   D   L   R   Y   V   D   Q   T   L   V   P   V   A   M   S   G   D   Q   G

3328 CGA CGT GTC GTC CAG CAG CGT CTG GGA TCG CGA GTA GCG AGA CAC CGG CCC CGC CTC CTT GCC CAC GGC GCA CGA CTG
    <  S   T   D   D   L   L   L   T   Q   S   R   S   Y   R   S   V   P   P   G   A   G   P   E   K   G   V   A   C   S   Q
```

FIG. 12C

```
3418 GAG CAG CGG GTC CAC CCG GAC CTG CTC CTG AAG CCC CAG AGA GTC CCC CAG TCG GTT GCT CGG CAC TAC GTT GCT CGG CAC CCG GTC CAG CAG
     <L  L  P  D  V  R  V  Q  E  Q  L  G  S  D  G  L  R  V  N  S  P  V  G  L  D  A  P  D  L  L

3508 GGC CTC CTG GAT CTC GCC GCC CCG GGA CCG CTC GGT AGA CGC CTC GGA CAT CGG CGC CGG GAG GTG
     <A  E  Q  G  I  E  T  R  G  S  R  E  P  E  T  S  A  R  W  G  D  V  W  S  M  P  P  A  L  H

3598 CCC GCC GGC GCC CCG GAC CGC GGC GAA GAC TAC CGA CGC CGC CAT CGC CGT ACG GCT GCG
     <G  G  A  R  G  G  V  A  F  V  S  L  V  A  L  V  A  A  A  A  M  A  T  R  R  S  R

3688 GCG GCG GGC GGC CCG GGC GAT GTC CGC CTC GGG CCA ACG GAC GTC CAT CCGTTCGGCGAACGTCAGGTCG TCA CGC
     <R  R  A  R  A  R  I  D  A  P  E  P  W  R  V  D  R  L  D  R  H  M        <  ·       A

3782 ATC GGC GGC CTC CTC CAG GTC AGA GAC GGC GAG GAG ACG CCC CGG GAC CGG
     <D  A  A  E  E  L  D  S  V  A  L  L  G  A  L  A  A  R  G  R  S  L  R  A  K  V  T  G  V  P

3872 GGC GGT CTC CCG CAC CTC GGC CAC CGG GTA GTG CAG GCG CTG CGC CTC CGG GGG CAG CAG CCG GCG
     <A  A  T  E  R  A  V  E  A  V  P  M  G  L  L  Y  H  L  A  I  A  T  R  Q  A  E  P  L  R  R

3962 TAG CGC CGC CAC CAC CTC CAG GCT GCT CGG CGT CAG CGC CCG GTA CGC CCG GCT ACG
     <L  A  A  V  V  E  L  T  A  T  S  P  A  P  V  S  E  P  A  G  H  R  L  Y  A  R  A  R  S  R

4052 CAT GCT GCG GGC CCA CCG GCT CAC CGC GAT CCG GCT CGC GCG CTC GTC CCC CGG TAC GGT CGG CCA GCG
     <M  S  R  W  R  S  V  A  I  R  S  A  V  V  R  L  W  G  E  P  D  D  Y  G  R  V  T  P  W  R

4142 CTG CCA TGC GCG CAT GTA CGC CTC CTG CAC GGC CTC CTG CGC GTC CTG CGC CTC GGC GTT TCC GGT GAT CAT GTA CAC GAA ACC CAG CAA TCG TTG
     <Q  W  A  R  I  Y  A  E  Q  V  A  D  Q  A  E  A  L  N  G  T  I  M  Y  V  F  G  L  L  R  Q

4232 CCG GCT GCC CCG GTA CTC GAA CTC CGC CTC GGC GTC CAT CCGCCACCTCCCGTGTCGCAGGGGACACGCCTGCGGGTCCCGGTTGCCCGGACCGG
     <R  S  G  R  Y  F  E  D  F  G  E  A  D  P  M

4338 CCGGCCTTCTTCCCTCCCGCGGGGGTTCCTCCTTCCCGGGGGTCTTCCCGGGAGGTGTCTGTCAGTGCAGCGCGCGCTCCGGTCGCTGCGCGCGCGGGGCCTTCGG

4459 CAGCGGAACAGGGACGACCGTCCGAGAATCGGGTGCCGCGCGAGTGGTGTCGGAGGCGCGGGGTGGGCGGTGG TCA GAC GTC GGT GAG CCC GGC GTC GGT GAG GAT CGG GCC GGC GGC
                                                                             <·  ·   V   T   L   G   A   D   T   L   I   P   G   A

4565 GAG CAG CAG GGC GCC GAC GGC GAG GCC GAC GGC CAG GCA GAC CAG GAA GAC CAG GAA CGG CGG GAA CGG CGT CAA CCG GGC
     <L  L  L  A  G  V  A  L  G  A  L  C  V  V  L  F  V  G  V  W  F  L  P  P  F  P  T  L  R  A
```

FIG.12D

```
4655 GAG CTG GTC GGC GTC GGA CTC CGG CAT CCG GCC ACG GCT GCG CAG CCG CTG CAA CTC GAT CAC GCC GCC GAA CAG CAG GAA
     <L   Q   D   A   D   S   E   P   M   R   G   R   S   R   L   R   Q   L   E   I   V   P   R   V   G   G   F   L   L   F

4745 CCA GAC CGA GGT CCA GGC GAA CGC CTG CAC CTG CGG CGG GTA CCA GGC GAA GAC GAC GAA ACC GCC GGT GGC GAG CAG CGA
     <W   V   S   T   W   A   F   A   A   Q   V   Q   P   P   A   Y   W   S   V   A   F   V   L   G   G   T   A   L   L   S

4835 CAG TGC CCC GTA GAC GTT GCG GAT CAT CGC GCC CAG CAG CAG CAT GGT CAT GCC CAG CCC GGT GAT CCG GTT CCC GGC
     <L   A   G   Y   V   N   R   I   M   A   L   M   A   L   L   V   T   V   S   L   M   T   I   R   N   G   A

4925 GAG CAG CCA CGC CCC GGC CAG GGC GAG GGC GAC GTA GGT CGG GGC GAA CAG GAT CAT GCC CAG CCC GGT GGG GCG GCC
     <L   L   W   A   G   A   L   G   L   L   T   P   A   V   Y   G   A   F   L   T   L   I   M   G   L   G   T   P   R   G

5015 GGC CGA CAG GGT GAG CCC GGA GGT GTC CGA GTG CAG CCG GAT GCC GCG CAG GGC GGC GGT GGC CAG CGC ATG ACC GCC
     <A   S   L   T   L   G   S   T   D   S   H   L   R   I   G   R   L   K   R   G   T   L   L   A   A   L   A   H   G   G

5105 CTC GTG GGC GAT CAC CGC GTT ACG CGC GAC CCG CCA GGG CAC CGC GGT GGC GGT GGC CAG GAC
     <E   H   A   I   T   V   A   N   R   A   V   R   W   P   V   R   T   A   V   L   A   V   A   T   A   L   V

5195 CAG CAG CGG CGG GTC CGG GGG TTG CGC GTC GCC GAG TTC GTT CCA GAC GCT CAG CGG GCC GTC GAT CAG GCC GCA GCC TAG
     <L   P   P   P   D   D   P   Q   A   G   V   L   E   N   W   V   S   L   G   D   I   L   D   V   P   G   C   G   I

5285 CGG CCC CGG CCC GGT CGC CGC GGT TCG CGC GCC GCG CCA CGG CGG TGC CCG GCC CGG TCG ACC AGC GCC GGG GCG CAC GCCGCCGGC
     <P   G   P   G   T   R   A   G   R   A   R   W   P   R   P   A   R   G   P   G   P   P   R   G   A   G   P   R   V

5378 TGACCGGCACCCGG TCA GGT CGC GGG CAC CCC GGT CGC GGG CAC GGT CAGC GTC GCC TGC GAC GAA GAA GGC CGC CGC TCT GGT GCC CAC CCG CAA CCG CCG CCG
                    <  •   T   A   P   V   G   T   L   D   G   A   V   F   F   A   A   A   R   T   G   V   R   L   R   R   R

5470 AGG GCG GAC CTC ACC GAC CGG CAC CTT GCG TCC ACG TCC ACG TAG GAC CAC GGA AGC GAC CCT GGT
     <P   R   V   E   G   V   P   P   V   K   R   G   R   L   V   V   A   L   V   G   T   P   P   L   V   S   A   V   R   T

5560 CAG CAT CCC GGG CAG GCC CTC CCC GGC CCG CTC CCC GTA GCT CGT CTG CCA GAC GTC GGT CAC GAC CAG GTC GGG GGT
     <L   M   G   P   L   G   E   G   A   R   E   G   Q   W   S   T   Q   E   G   Y   P   L   D   T   V   L   D   P   T

5650 CAT GCC CGC GAC CGC GGC CTC GGT GAG GGC GTC GAA CAC GCG GCC CGG CAG CGG GCC TGC CGC GTC CAG
     <M   G   A   V   A   E   T   L   A   V   R   D   F   V   D   A   R   R   V   A   Y   P   L   P   G   G   A   A   D   L
```

FIG.12E

```
5740 ACG GCC GCG CAG CCG GTG GGC GGC GGC CGC CTC CGC GTA GTG CGG CTT GTC GAA CGC CTC GGC GCG TTG CGC CAG CTC GCG GGC CCG
     <R   A   R   L   R   H   A   A   A   A   E   A   Y   H   P   K   D   F   A   E   A   R   Q   A   L   E   R   A   R

5830 CGT GTC GAG CCC GCC GCC GGT CAG CAG GCC GAG GTT GGC GCC AAG GTC GAG CGC CTC GAC GTC GGA GGC GAG CAG CCC GGC
     <T   D   L   G   A   G   T   L   G   L   N   A   R   A   L   D   L   A   A   E   D   V   D   S   A   L   L   G   A

5920 AAG GCT CGG CAG GTG CAG GAG CAC CGT CAG GTA CAG CAC CTC CTT TAT GGC TCA GGC TGC TGC CCA GAC TGG GTC ACC GCA AGT CCT CCG
     <L   S   P   R   H   L   L   A   L   V   T   L   L   Y   G   S   G   C   C   P   D   W   V   T   A   P   S   T   P

6010 GCG CAA CTC CAG GCG GTG TTG CAG GAC CTC GGA GGC GAG CGC CGG CGA GCG CAA CAC GGC GCC ACT
     <R   L   E   L   A   T   Q   L   V   E   S   A   L   R   V   P   F   A   P   F   G   P   A   S   R   L   V   A   G   S

6100 GGC CAG GTC GCC GTA CGC ACC GCG TAC GGT TTC GTG CCG GTA AGT CAC ATG CCC TCC GCG CAC CCT ACC AAT CCG GCA CCG CCG GGC
     <A   L   D   G   Y   A   G   R   V   T   E   H   R   Y   T   V

6190 CGG G TCA GGC CGC AGG CCG GGA CTC GAT CCA GTG GAA GTC GGT GGG GGA CAG CGG CGT GAC GTC CTC CAG GAC GTC CTC GGA CAG CCC CGC CTT GCC GCA CAG
     <  •  A   P   R   S   E   I   W   H   F   D   T   P   P   L   P   T   V   D   E   L   S   L   G   A   K   G   C   L

6281 CCG TTC CAG GTC GCC TCG GGT CCG CTC CAG GCC CTG CCC GTT GAC CAG CAT CCC CAC GTC GGT CAG CGC CAG GTT GGC CGC CGG
     <R   E   L   D   G   R   T   R   E   L   G   Q   G   N   V   L   M   G   V   D   T   L   Y   A   L   A   N   A   A   P

6371 GCC GAC GTC CGG CAG CAG CAC GTG GTC GAT CAT GAC CGG GAC GAC GTG CCG GGC GAG GAT TCC CGT CGC
     <G   V   V   D   P   L   V   H   D   I   M   V   I   R   G   G   P   A   V   E   A   C   H   R   L   I   G   T   A

6461 CCG CGC GTC GCC CCA ACC GTG GAT CAC ACT TTT GAG CAG CAG GTC GAG GAG GAC GTC ACC CAC CTC GAT
     <R   C   R   D   G   V   G   A   R   R   L   N   G   A   A   E   A   S   G   S   A   S   D   Y   L   V   G   R   V   G

6551 CCG GCA CCG GTC GCC GAC GTC GGG GCG GCG GCG CAG GTT CCC GGC GCT CTC GTA GAG GCC CCG CAC GCC
     <R   D   G   W   G   H   I   V   S   K   L   L   Y   L   D   A   D   A   P   V   R   E   F   F   D   G   V   E   I

6641 GGG GTT CGC GCC GAG GCC GGC GGC CAG CAG GGT GCC GTC GAC CAC CGT GTC GAT CGC GTT CAG GTC GGG TCG CCC CAC CGC CTC
     <P   N   A   A   L   V   A   L   L   T   G   D   G   G   G   V   D   V   V   T   R   V   G   A   L   D   T   R   E

6731 GGC AAC GGC CGC GCC GAC GAC CTG GGT GCT GTG CTC GCT CTG CAT CAC CCC GGC GGT GTA CTC GAA
     <A   V   A   A   A   V   S   H   T   V   Q   S   M   A   A   N   Y   L   E   S   L   D   P   R   G   G   V   Y   S   F
```

FIG.12F

6821 GAA GTC GGT GCC GAA GAT GCC GTC CCA GGC CGG GGT GGT CAT GGC CGG GTC
     < F   D   T   G   F   I   G   D   F   A   P   E   G   T   R   V   S   H   A   L   G   D   W   A   T   T   M   A   P   D

6911 GGT CAG CAT CCC CAG CAG CCG CAG TCG GTC CCC ACG CAG CGC GGG GAG CGC GGG TGT
     < T   L   M   R   A   L   P   R   L   T   G   P   R   D   G   R   L   L   A   G   M   P   A   L   A   F   R   G   P   T

7001 GGT CTC GAG CAC CCG CAG GGC CAG CAT GTC GGC TCG CGC GTC CGC GAA CAC CTC CTG
     < T   E   T   L   V   R   L   A   L   A   R   L   V   R   F   M   T   D   A   R   A   D   Y   R   L   A   L   E   Q

7091 CGG GGT GCG CTC CTC GTC GCC GAT CGC CGC GGG CAG CCC GCC CAT CCC GCC GAA CAC CAA
     < P   T   R   E   D   D   G   I   A   D   P   L   G   L   R   V   C   Y   G   V   L   R   S   A   M   G   G   F   V   L

7181 CCG CAT CAG CTC CGG CCA GGC GTC CGC GGC CTG CGC GCG CCG GGT CGT GGC
     < R   M   L   E   P   W   A   A   D   A   G   T   Q   A   R   R   A   S   P   E   D   T   T   T   A   R   E   D   T   D   P   V

7276 CGG TCA TCG GAC CTC CGG CCG CGA GTA GTC GAC GTC GCC CGG CTC GCC GTC GCG GCG GTC CAG CC GCTCGTCGTCGTGTCCGGGA
     < T   M

     < V   R   V   P   E   A   A   P   L   G   L   G   I   R   V   A   R   E   V   P   S   Y   D   G   D   P   R   D   L

7366 GTC CAG CTC GCC CAC CGG CTG CAG GCT CGG GGT GCC CAT GGT GTT GCC CCG GGT GTG CGC CAC CGG GAA CGG
     < D   L   E   G   V   P   Q   L   S   P   Q   A   M   F   R   P   R   T   G   T   N   A   V   P   T   H   V   L   F   P

7456 GTG GCA CAG GTA GAC ACC GTC GGC GCG TCC GGT GGC GGA GGC GAG CGG GTC GAG GTA GGT GCC CTC
     < H   C   L   Y   V   D   G   A   R   G   T   A   S   A   L   P   R   D   R   G   V   D   G   V   D   L   Y   T   G   E

7546 CGG GCC GTA CGG TTC GAG CAG CAG CAG GGC CGG CGG CAC GTC CTC GTC CCG GGT GTC GGA GAA
     < P   G   Y   P   E   L   L   P   P   V   D   L   H   S   G   V   R   V   L   T   P   A   E   R   E   D   T   D   S   F

7636 GAG GAA CAG CAG GCC CAG CCG CTG GGG GCC CGA CCG GAG GTT GCA GCG GAG GTC CAG GTC CTC CGG GCG
     < L   F   L   L   L   A   R   G   S   R   L   N   C   R   F   V   E   A   Y   N   P   P   V   L   D   L   E   G

7726 CTC CCA GTT CTG GGG GCC CAG CGG CTG GGC GTC GTC CGC GAA ACT GGC GTC GAT GTC CTC CGG GCG
     < E   W   N   Q   P   G   L   R   Q   A   D   D   A   L   F   S   A   D   I   H   W   G   Y   D   E   T   Q   E   P   R

7816 CTT GGG CAC GTA CCG GCC CGG GAA CCG GAC GAT GCC GAT CCA CGG CTT CAA CGG GTC GGC GGC GTG
     < K   P   V   P   F   R   V   P   F   T   G   I   R   D   L   P   K   W   R   G   V   G   V   L   Q   D   F   A   A   H

FIG.12G

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7906 CAG CCG GGG CGT GGT GCT GCG CAC GAA GGG CTC GTC CTG GAG GCC CAG GGT GCT CCG GTC CTC
    < L   R   P   T   T   A   S   R   V   F   P   E   A   D   Q   L   G   L   R   V   E   R   S   W   T   S   R   D   E

7996 GGG GTC CAT GCC GAG TTG CCG CCA CAG CAG TTC GCG GAG CTC CGC CTC CAA CTT CAC GAA CCC GTC
    < P   D   M   G   L   Q   R   W   L   L   E   R   G   Q   A   L   E   A   P   F   A   E   L   K   V   F   G   D

8086 GGA GAC GAA CCG CTC GTC GCT GAC CTG GGC GCT CAT ACT CCT TCC CGG TTC CCG AGG AGC GAG ACG
    < S   V   F   R   E   V   Q   E   D   S   L   V   Q   A   S   M

8176 GTC GCA CCC GCG GGA ACC CTG GCG CCT CAA CGT CGT CAA GAT TCG CCA GGT TGA ATG GTA GAC AAG CCG CCA CCG TCA GGG ACT AAC
                                                                        < * P   S   V

8266 GTT TTC CTC AGC ATC GTC CGG GCC ACC GCG AGA GCG CCG GGC CGC TCG GCT CTC CCC GGG TGC GGC GAT
    < N   E   A   D   D   P   G   G   R   S   R   R   V   G   R   E   V   R   L   W   R   S   E   G   P   A   A   I

8356 GCC GTC GAG CCG GGC GCG CTC GTC CGC CTC CGG GTC CAG CGC CTG CAG GCG GGG GCC GAC
    < G   D   L   R   A   R   A   E   E   P   L   P   R   D   A   A   L   A   R   A   Q   D   L   T   R   P   G   V

8446 GAC CGT GGT GCT CGG CAC CGG GCA CAC GGA CAG GCC CAG GCC CTC GAC GGC CAC CTT CGC CAA
    < V   T   S   T   V   G   P   A   D   Y   V   W   A   H   A   L   D   P   L   S   G   L   E   V   A   V   K   A   L

8536 CCG GCC CAG GGT CCG CCA CAC CGG CGA GTG GGC GCC CGG GAA CCG GTC GCG GGG CGG CTC GCC GTC
    < R   G   L   T   R   W   V   P   Q   W   H   P   G   S   P   A   Y   W   A   T   F   R   A   D   R   P   P   E   G   D

8626 GGC GAA CCG GTC GGA GAG CAG ACC CAT CGC CAG CGG GCT GTA GGT GAA CAG CGG CGG CAG CAC GTC CCG
    < A   F   R   D   S   L   G   M   A   L   P   S   Y   T   F   L   G   L   G   Y   E   A   C   L   P   L   V   D   R   I

8716 CTC GAT CTC GCG GGG CAC CTC GTC GTT GTA CGG GCC CGA CTG CTC GGC GGA CTG CGC GCG CAG GTC GAC
    < E   I   E   R   E   L   L   N   Y   P   S   Q   E   A   V   V   P   A   A   G   R   S   Q   A   T   R   L   L   D   V

8806 GAT CCG GCC CCA GCT GGG CAC CAG CCG CTG GCC CGG GTC CGT GGG CAC GGT GCC CAC GTA GCG GAC CTT
    < I   R   W   S   P   V   T   G   L   R   P   Q   D   A   L   E   Y   A   T   P   V   T   S   T   G   V   R   V   K

8896 GCC CGA GCG GAC CAG GTC GTC GGC GGA CAC CGT CTC CTC CAC CGT GTC AGT GCG GAC CAG CAG GTC GAT GTG H
    < G   S   R   V   L   D   D   L   A   S   V   T   E   E   V   P   T   D   P   D   H   R   H   L   Y   L   L   D   I   H
```

FIG.12H

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8986  GTC GGT ACC CAG CCG GCG CAA CGA CTC CCG CTT CAG GGC CTC GCA CTC CCG GTA CGC CGA GGT GCC CCG GTC GTT CGG TCC CGG GCC GAC CGG
       <D   T   G   L   R   R   L   S   R   E   C   E   R   K   L   A   Y   A   S   T   G   R   D   N   P   G   P   G   V   P

9076  ATT GAA GAT CTT GGT GGC CAG CAG GAC GTC CCG GCA GCT CCG CAC GTC GCT GCG GCC GTC CTG GTA GAC
       <N   F   I   K   T   A   L   L   V   D   D   R   C   S   R   V   A   A   G   V   I   E   E   S   R   G   D   Q   Y   V

9166  GTT GGC CGT GTC GAC GAG GTT GAC TCC CGC GGC GAC GAT GGC CGT GGC GAC CTC CGG CTG GCC CGG GCC GAA GTT
       <N   A   T   D   V   L   N   V   G   A   E   V   A   T   A   V   I   R   A   A   E   E   P   G   T   P   G   G   F   N

9256  GAA CGC CCC CAG GGA CAC CTT GGA CAC GCC CAA CTG TCG GTA CTC CAC GCTGCCCTCCCCTGCGGTGGTCGCCGGCCACCC
       <F   A   G   L   S   V   K   S   V   R   L   G   C   R   G   L   Q   R   Y   E   V

9355  CGTCGTGCGGCCGGTGCTCCCCGAGCCGGGAGTGGCCGATCTCGATGGGGGAGCCTAGTACCGGCGCGGGTGCCTCGGCCGTGGTACTAGCAGAACTGCTAG AGC ATC CGT CGA
                                                                                                                   >M   S   D   K   Y   G   R   S   A   L   W   E   R   Y   N   S   T   Q   V   T   E   E   A   A   D

9470  GCC GCC GGG CGG CGG AGC GGC TAC GGT GTG CCT GAA CCC CGC CGG ACC ACG GGC GTC GAC GAG GCG ATC GAG CTG
       >D   L   T   S   F   K   S   S   D   V   N   Y   K   L   A   L   W   D   P   R   V   S   G   V   R   Y   L   K   T   L

9560  ATC GGC GGG GAG GAG GCG GGG ATG AGC GAC AAG TAC GGG GTC AGC GGG GTC CGC TAC CTG AAG ACG CTC
       >I   F   N   L   A   E   N   L   G   E   A   N   R   A   R   L   R   R   I   A   N   R   D   V   G   D   P   I   S   V

9650  GAC CTC ACC TCC TTC AAG TCG AGC GAC GTC AAC TAC AAG CTC GCC CGG GTC AGC GGG GTC CGC TAC CTG AAG ACG CTC
       >D   L   T   S   F   K   S   S   D   V   N   Y   K   L   A   L   W   D   P   R   V   S   G   V   R   Y   L   K   T   L

9740  ATC TTC AAC CTG GCC GAG AAC CTG GGC GAG GCG AAC CGG TTG CGC GGC GAC GTC GGC GAC ATC TCC GTC
       >I   F   N   L   A   E   N   L   G   E   A   N   R   A   R   L   R   R   I   A   N   R   D   V   G   D   P   I   S   V

9830  GTC TGG GAC GGC GAC CGG ATC TGC ATG GAC TAT CTC CAG GCG GTG CCA CTG GAC GGC GCG
       >V   W   D   G   D   R   I   C   M   D   Y   L   Q   A   V   L   E   L   E   F   F   S   R   H   V   P   L   D   G   A

9920  ACG GTG CTG GAG ATC GGC GCT CTG GCC CGC TAC GGC CGC CGC TAC CTG CGC GAG AGG GTC CAC TTC CAC GTG GTC GAC CTG
       >T   V   L   E   I   G   A   G   Y   G   R   T   C   H   A   V   L   S   N   H   D   V   A   A   Y   H   V   V   D   L

10010 CCG AAC TCC CTC GCT CTG GCC CGC CGC TAC CTG CGC GAC CTC GTG ATC AAC ATC GAC TCG TTC GCG GAG ACG GTG CGC GCG TAC
       >P   N   S   L   A   L   A   R   R   Y   L   G   T   V   L   T   A   E   Q   L   A   R   V   H   F   H   G   V   G   E

10100 GTG GAC GGG CTG CCG AGC GAG CTG CGC TAC GAC CTC GTG ATC AAC ATC GAC TCG TTC GCG GAG ACG GTG CGC GCG TAC
       >V   D   G   P   L   S   E   L   R   Y   D   L   V   I   N   I   D   S   F   A   E   M   T   A   E   T   V   R   A   Y
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FIG.12I

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10190 CTC GCC TTC GTC GCC ACC AGG GCC CGC CAC CTG TAC GTC AAC AAC CCC GTC GGG AAG TAC CTC GAC AAG ACC CTG GAC GGG CAC TTC CAG
      > L   A   F   V   A   T   R   A   R   H   L   Y   V   N   N   P   V   G   K   Y   L   D   K   S   L   D   G   H   F   Q

10280 GGC GAG GAG GTG GCC AAC CTT GCG GTC AGC CTG ACC GGC CTG CGC GAC GTC GAC CAG AAC CAG GCC GTG CGG CGG CAG TCC
      > G   E   A   V   V   N   L   S   T   G   L   L   R   D   V   I   D   I   H   D   N   Q   A   V   R   R   Q   S

10370 CGG GCG TTC CTC GAC GCC TAC CGG CCG GGG CCG TGG GCC TGC GTG GCC GAG AGC CGG ACG ATC CCG TGG ACC TAC TAC TGG CAG GCG
      > R   A   F   L   D   A   Y   R   P   G   P   W   A   C   V   A   E   S   R   T   I   P   W   S   Y   Y   W   Q   A

10460 CTC TAC CGG GCC GAG GCG GAG GCG GCA CCC GGG CGG GAT TGA GGTGACCGGCGAGCGGGGAGCCCGGACCGGCCCGTCGTCGGCGTCCTCGGCGGCCTCC
      > L   Y   R   A   V   E   A   A   P   A   P   G   R   D   .

10566 GGCCTGGTCGGCACCGCT GTG CTG GCC GCG CTC GCC GAC CGG GCC GTC ACC GTC CGG GCC CGC GCG
                       > V   L   A   A   L   A   D   R   A   V   T   V   R   A   V   A   R   R   A   A   V   L   P   A   A

10659 CCG GGC CGC GCG TTT GAG GTG GTA CGG GAC CTG GCG GGA GCC CTG GCG GCG GTA CGC GAC ACG GCC GTG GTC
      > P   G   R   A   F   E   V   V   R   A   D   L   T   D   R   G   A   L   A   A   A   V   R   D   A   T   A   V   V

10749 AAC CTC ACC CTG GAC GTC TCG GGC TGG CGG GGC GAC GAC GAC GAC CGG GTC AAC GAG CTC GTC GGG
      > N   L   T   L   D   S   S   G   W   R   G   A   D   D   D   R   S   A   R   V   N   V   E   L   T   R   E   L   V   G

10839 ATG CTC CGC CGG CCC GGG CCG ACG GGC ACC ACA CTG GTC TTC GCC GGC TCC GCC CAG AGC CAG GCC GTG CCG CGG GCC ATC
      > M   L   R   P   G   P   G   G   T   P   T   T   L   V   F   A   G   S   A   S   Q   V   G   R   P   P   R   I   P   I

10929 GAC GGC ACC GAG CCG GAC CAC CAC CCG GCC ACC CCG TAC GAC CGG CAG AAG CAG GCG GAG TCG CTG GTC GTG GCC GGG GCC GGC
      > D   G   T   E   P   D   H   P   A   T   P   Y   D   R   Q   K   Q   A   A   E   S   L   V   V   A   A   T   G   A   G

11019 GTC GTG AAC GGC GTG TCG CTG CGA CTG CCA CTG GTG TTC GGG CCG GTG CCG CCG GGA GCC GGG GAC CGG GGC GTG GTG TCC ACG ATG
      > V   V   N   G   V   S   L   R   L   P   T   V   F   G   P   V   P   P   G   A   G   P   D   R   G   V   V   S   T   M

11109 ATC CGC CGG GCG CTG TCC GGA GCG CCA CTG ACC ATG TGG CAC GAC GGG CGG GTG CAA CGG CAG CTG CTG TAC GTG GCC GAC GCC GCC
      > I   R   R   A   L   S   G   A   P   L   T   M   W   H   D   G   R   V   Q   R   Q   L   L   Y   V   A   D   A   A   A

11199 GCC TTC GTG GCG GCG CTG GAC GAC CAC CCC GGG GCG CTG ACC GGC CGG CAC TGG CCG CTC GGC GAC GGT GAA CGG GGC CTC GGG GAC CTG
      > A   F   V   A   A   L   D   H   P   G   A   L   T   G   R   H   W   P   L   G   D   G   R   G   E   R   L   G   D   L
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FIG.12J

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11289 TTC CGC GCC ATC GCC GCC CTG GTG GCC GAG CGG ACC GGT CGG CCA CCG GTG CCG GTG CTG GCC GTG CCC GAC GAG GCC CGG GTC
      >F   R   A   I   A   A   L   V   A   E   R   T   G   R   P   P   V   P   V   L   A   V   P   P   P   D   E   A   R   V

11379 AGC GAC TTC CAC GAC ATG GTT GAC GTC GTT GAC TTC GCC TCG GCC TTC CAG GCG GTC ACC GGG TGG GCG CCC CGG GTG CCG TTG CGC CTC GCG CTG GAC
      >S   D   F   H   D   M   V   D   A   S   A   F   Q   A   V   T   G   W   A   P   R   V   P   L   R   L   A   L   D

11469 CGC ACC GTC GCG GCG CTC GCC CGC GAC AGC GAC GAC AGC GGG CCC GAG GCC CCG GCG GTC GGC CCG GAT CAG GCC CGG
      >R   T   V   A   A   L   A   R   D   D   S   G   P   E   A   P   G   G   G   V   G   P   T   R   A   D   Q   A   R

11553 AAG CCG GAC TCG ATC TCC AGG CAG GTC CGG TAG TCGGGCAGCAACCCACGGGGCGAGCGCCTGGTCGAAGGTGATCGGCGGTGCGGTCCCGCTCCGACCAGGATCGGTTCGAC
      >K   P   D   S   I   S   R   Q   V   R   .

11663 GTCCTCGGGGATGGGCAGGCCCAGCCCGGGGGTCGAGCGGCCAGTTCGTTCTCGAAGACGTACTCCTGGGACAGGAGCGTACGACATGACGGTGTCGGCGCAGGGCGACGAAC
11784 ATGTGCGGCGACCCGACCGGCAGGTAGACACGGGCAGCCACCGCGAACTGGTCGTGTGAGCTGGAACTCCTCGCTGTGCGAACGCTGGTCGGTCGAGGAGAGACCAGGTCGAGCGACCC
11905 GGCCGGTGCCGGGCGAGGAGGACGAACTTCGGCGGTGCCGGCGGGGGTGAGGTGCAGCGCCGTGTAGCTGGTCTGCCGCCGACGGGGAACAGCGGGTA
12026 CCCGACCGGTGTCCCGGAACCAACGAGTGCGAGATACGGGCGAGAGGAACACCCCCGGTAGTCGTCGGGGTAGAACGGGGTAGAACGGGTAGCCCTTCAGCGGTAGCGGGCGGGGACACC
12147 GGCGGG
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FIG.12K